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ASSESSMENT OF COMBINING ABILITY AND GENE INTERACTION IN MAIZE (*ZEA MAYS* L.) FOR SUPERIOR PARENTAL COMBINATIONS IN NORTHWEST INDIA

Mudamala Syam Kishore Reddy[1], Harshita Thota[1]*, Vineet Pawan[2] and I.R. Delvadiya[3]

[1]Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional Univ., Phagwara-144001 (Punjab), India.
[2]Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology (GBPUA & T),
Pantnagar - 263 145 (Uttarakhand), India.
[3]Department of Genetics and Plant Breeding, School of Agriculture, Dr. Subhash University, Junagadh - 362 001 (Gujarat), India.
*Corresponding author E-mail : harshitarao400@gmail.com

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ABSTRACT

Tests for combining ability and gene action in maize were conducted using 56 single crossings, 8 lines, 7 testers and 1 standard check. Eleven traits, including Days to 50% Tasselling, Days to 50% Silking, Days to Maturity, Plant Height, Ear Height, Ear Length, Ear Girth, Number of Kernel Rows per Ear, Number of Kernels per Row, 100-Kernel Weight, and Grain Yield per Plant, showed highly significant mean squares attributable to genotypes, parents, and hybrids. These results demonstrated substantial genetic diversity. Notably, significant mean squares post-variance analysis of GCA and SCA indicated that additive and non-additive genetic variants influenced every characteristic. In particular, high, or medium GCA for yield component qualities in the majority of parents were linked to substantial GCA effects for grain yield per plant, whereas deficits in these traits were shown in poor combiners. Only a small number of cross combinations showed significant SCA impacts; these combinations worked well for particular yield-related traits. Several features appropriate for general combiners were found using inbred line GCA effects, indicating their potential for recurrent selection-based synthetic variety creation. Notably, crosses involving parents skilled in either exceptional features or general combining ability produced hybrids with notable SCA effects. Further study and use of these hybrids in single cross hybrid combinations appear promising. Because non-additive genes predominate in crossings with significant SCA effects, there is potential for heterosis breeding in these crosses.

Key words : Inbreds, L x T, GCA, SCA, Gene action, Maize.

Introduction

Zea mays L., or maize as it is formally known, is an important staple crop in the world's agricultural system. Its importance extends to the manufacturing of consumer items, animal feed, and human nutrition. Among cereal crops, maize stands out for its versatility in a range of climates, seasons, and applications. Waxy corn, high amylase corn, high oil corn, excellent protein corn, baby corn, popcorn, standard yellow or white grain maize, and many other varieties are among them (Shruti kritika *et al*., 2022). As a C4 plant, maize efficiently captures energy and exhibits a high potential for grain production per unit area compared to other cereals. Maize grain composition typically comprises approximately 10 percent protein, 4 percent oil, 70 percent carbohydrates, 2.3 percent crude Fibers, 10.4 percent albuminoids, and 1.4 percent ash. Additionally, maize contains sufficient levels of carotenoids, various vitamins, and minerals. The notion of "combining ability" has become more important in maize breeding research due to the growing demand for maize, which highlights the urgent need to increase its productivity and adaptability. Acknowledged as the "queen of cereals," maize is an essential part of global agriculture and will always require efforts to increase both its productivity and quality. The investigation of combining ability is of great interest because it plays a crucial role in elucidating the complex genetic foundations of characteristics that are difficult to manage, hence facilitating the successful resolution of issues brought about by a fast-changing agricultural environment. It is possible to see a paradigm shift in maize breeding history from a solitary dependence on additive genetic effects to an appreciation of the critical roles played by non-additive variables like dominance and epistasis. General combining capacity (GCA) and specific combining ability (SCA), which were first proposed by Sprague and Tatum (1942) provided the foundation for understanding the complex connections between genes that are necessary to maximize breeding tactics. Maize's complex genetic makeup makes it a difficult crop to grow, thus it is important to look closely at how different genotypes interact to produce desirable features in hybrid offspring (Erenstein *et al*., 2020). In maize heterosis may be used by developing and identifying high-performance vigorous parental lines and evaluating their cross-combination capacity to discover hybrids with strong heterotic effects. Maize productivity development focuses on grain production and maturity. The heterotic patterns and combining abilities of parents and crossings help breeders choose and generate single cross hybrids. This study aimed to measure maize combining capabilities, focusing on grain yield and maturity.

Combining ability analysis stands as a pivotal tool in contemporary maize breeding, addressing the pressing challenges of modern agriculture. With maize serving as a vital staple crop globally, the demand for high-yielding and resilient varieties escalates. Through the assessment of general combining ability (GCA) and specific combining ability (SCA) effects, breeders can distinguish between additive and non-additive genetic contributions to hybrid performance, strategically selecting parental lines with favourable GCA for desired traits. This methodological approach, as highlighted by Wu *et al.* (2022), facilitates the creation of hybrids that consistently surpass parental performance in terms of yield, disease resistance, and stress tolerance, crucial attributes amidst evolving climatic patterns and agricultural needs.

In addition, integrating ability analysis is crucial for directly tackling the worldwide problem of food security, going beyond its scientific significance. Additionally, this kind of analysis helps in the development of hybrids of maize that are more resilient to stress, which is crucial for reducing the effects of climate change and erratic weather. To put it briefly, ability analysis combined with maize breeding greatly contributes to scientific knowledge while also supporting sustainable agriculture and providing food for a growing population.

Materials and methods

The study conducted at LPU in Punjab utilized a randomized block design with three replications for planting inbred lines. Data was collected during the 2023 *kharif* seasons for 56 single crosses involving 15 parents and one standard check. Eleven yield traits were measured, including days to 50% tasselling (50% DT), days to 50% silking (50% DS), days to maturity (DM), plant height (PH), ear height (EH), ear length (EL), ear girth (EG), number of kernel rows per ear (NKRE), number of kernels per row (NKPR), 100-kernel weight (KW), grain yield per plant (GYP). The Line x Tester analysis, introduced by Kempthorne in (1957), assessed GCA and SCA for parent selection and understanding genetic mechanisms controlling quantitative traits.

In this total 15 genotypes of 8 lines (BPPTI34, BPPT135, BPPT144, HKI1332, BML6, HKI586, HKI295 and HKI323-8), 7 testers (BML22, BML20, BML15, BML14, BML8, BML3, HKI335 and DHM117) and 1 check (DHM117) are collected from CIMMYT, Hyderabad and check from ANGRAU, Hyderabad (Table 1).

The study employed data suggested by Sprague and Tatum (1942) for parents and hybrids in combining ability analysis. The analysis focused on dividing variance into general combining ability (*gca*) and specific combining ability (*sca*) components based on a statistical model.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + (1/b)\, e_{ijk}$$

Table 1 : List of Parents and Check.

Number	Genotypes	Category	Source
Line 1	BPPTI34	Inbred line	CIMMYT, Hyderabad
Line 2	BPPT135	Inbred line	CIMMYT, Hyderabad
Line 3	BPPT144	Inbred line	CIMMYT, Hyderabad
Line 4	HKI1332	Inbred line	CIMMYT, Hyderabad
Line 5	BML6	Inbred line	CIMMYT, Hyderabad
Line 6	HKI586	Inbred line	CIMMYT, Hyderabad
Line 7	HKI295	Inbred line	CIMMYT, Hyderabad
Line 8	HKI323-8	Inbred line	CIMMYT, Hyderabad
Tester 1	BML22	Inbred line	CIMMYT, Hyderabad
Tester 2	BML20	Inbred line	CIMMYT, Hyderabad
Tester 3	BML15	Inbred line	CIMMYT, Hyderabad
Tester 4	BML14	Inbred line	CIMMYT, Hyderabad
Tester 5	BML8	Inbred line	CIMMYT, Hyderabad
Tester 6	BML3	Inbred line	CIMMYT, Hyderabad
Tester 7	HKI335	Inbred line	CIMMYT, Hyderabad
Check 1	DHM117	Hybrid	ANGRAU, Hyderabad

Results and Discussion

Genetic variability, except in parental ear length and grain yield per plant, underscores maize productivity's genetic factors. Crosses show significant mean squares, indicating additive and non-additive genetic influences, as noted by Kamara (2015). Plant height and grain yield per plant exhibit higher SCA variance than GCA, reflecting non-additive gene action dominance. Conversely, traits like the number of kernel rows per ear demonstrate higher GCA variance, suggesting additive gene action predominance. Kempthorne's (1957) emphasize the relevance of dominant gene activity in trait expression by highlighting its influence on characteristics like ear length and days to maturity.

Variance components determined narrow sense heritability, ranging from 29.14% to 78.17% (Table 3). Days to maturity had low heritability, suggesting minimal additive gene influence. Moderate heritability was observed for days to 50% tasselling, days to 50% silking, ear traits, and the number of kernel rows per ear. Significant heritability was found in plant height, number of kernels per row, 100-kernel weight, and grain production, indicating both additive and non-additive gene actions. Previous studies highlighted both gene activities (Subba *et al*., 2022 and Abd El-Latif *et al*., 2023).

The examination of combing ability demonstrated that the variation assigned to Specific Combining Ability (σ^2s) was larger than the variance attributed to General Combining Ability (σ^2g). For every feature examined in the F_1 generation, the degree of dominance exceeded unity (>1) and the dominant genetic variance (σ^2D) outperformed the additive genetic variance (σ^2A). The predictability ratio for every feature in the F_1 generation, on the other hand, was less than unity (<1). These results imply that non-additive gene activity predominates in all attributes.

The study highlights non-additive gene action's crucial role in yield and related traits, influenced by epistatic interactions or dominance effects. Ongoing heterozygosity necessitates continued selection, particularly for traits controlled by non-additive genetic variation like days to maturity, plant height, and ear length. Leveraging hybridization and advanced methods, such as heterosis breeding, can exploit these effects to improve maize breeding (Abd El-Latif *et al*., 2020 and Aly *et al*., 2022).

The GCA effect variance for each parent across eleven traits is illustrated in Fig. 1. The study aimed for positive GCA impacts in most traits, except for Days to 50% Tasselling, Days to 50% Silking, Days to Maturity, and Plant Height, desiring negative characteristics. Not all parents had substantial GCA impacts in the intended direction for all characteristics. Poor grain yield combiners also performed poorly in other components. High grain yield GCA correlated with high or average GCA for various traits, especially in BPPT135, HKI1332 and BML15. Specific lines like BPPT135, HKI586, BML14 and HKI335 exhibited negative GCA impact for early silking, while HKI1332 and HKI295 showed negative GCA influence for early maturity. These negative GCA values suggest effective combinations for earliness, consistent with prior studies by Aung *et al*. (2016), Chandel *et al*. (2019) and Chinthiya *et al*. (2019).

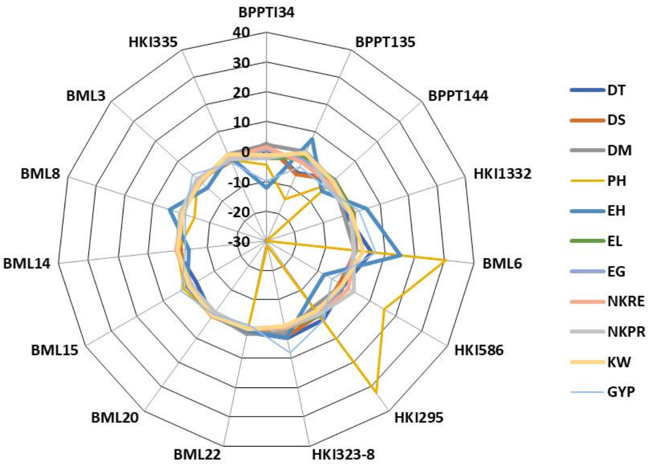

Fig. 1 : Estimates of GCA effects of parents for eleven traits in maize.

Parents like BPPTI34, BPPT135, HKI1332, HKI323-8, and BML8 show effective negative GCA for plant height, while positive GCA for ear height is seen in BPPT135, HKI1332, BML6, HKI323-8 and BML8. These parents, with negative GCA for plant height and positive GCA for ear height, are versatile combiners for both traits (Chozin *et al*., 2017 and Ismail *et al*., 2024). Substantial positive GCA effects are observed in BPPT134, BPPT144, BML22 and BML20 for ear girth, while BPPT134, HKI586, BML14 and HKI335 show strong positive GCA for kernel rows per ear. Highly significant positive GCA values for 100-kernel weight are shown by BPPT135, BML6, BML20 and HKI335, indicating their proficiency as good combiners. In line with earlier maize research findings, the parents HKI1332, BML6, HKI295, HKI323-8, BML15 and BML3 show extremely substantial favourable GCA impacts for grain production per plant (Abd El-Azeem *et al*., 2021; Diviya *et al*., 2022 and Kamal *et al*., 2023).

Significant GCA effects favour grain yield, despite negative impacts on earliness and plant height. BPPT135 stands out as the top general combiner, exhibiting positive

Table 2 : Analysis of variance of L X T mating design including parents in F_1 generation.

Source of Variation					
Characters	**Replications**	**Lines**	**Testers**	**Crosses**	**Line x Tester Effect**
D.F	**2**	**7**	**6**	**55**	**42**
50% DT	0.30	17.61**	9.30**	55.13**	27.57**
50% DS	0.79	18.83**	8.93	38.80**	25.66**
DM	3.01	14.07*	9.23	41.47**	34.92**
PH (cm)	172.7*	71.58	281.12**	2078.54**	622.25**
EH (cm)	31.84	114.44**	152.48**	405.69**	208.10**
EL (cm)	0.08	0.76	0.50	6.90**	4.65**
EG (cm)	0.16	0.17	0.37**	1.137**	0.75**
NKRE	2.60**	6.24**	1.67	7.32**	4.53**
NKPR	8.06	4.87*	6.50**	17.50**	4.92**
KW (g)	0.27	2.43**	2.82**	9.74**	2.38**
GYP (g)	33.28	20.04	30.35	153.36**	49.31**

*, ** Significant at 5 and 1 per cent probability levels, respectively.

Table 3 : Variance components, dominance, additive effects, and heritability for 11 traits in maize.

Characters	gca variance (σ^2g)	sca variance (σ^2s)	Average degree of dominance	Predictability ratio ($2\sigma^2$ g/$2\sigma^2$ g+σ^2 s)	σ^2A	σ^2D	Heritability (ns)
Days to 50% tasselling	5.96**	8.37**	0.83	1.42	11.93	8.37	56.48
Days to 50% silking	3.19**	6.98**	1.04	0.91	6.38	6.98	42.72
Days to maturity	2.39**	9.55**	1.41	0.50	4.79	9.55	29.14
Plant height (cm)	278.58**	194.37**	0.59	2.86	557.16	194.37	72.87
Ear height (cm)	42.59**	61.16**	0.84	1.39	85.18	61.16	55.11
Ear length (cm)	0.55**	1.24**	1.05	0.89	1.11	1.24	41.09
Ear grith (cm)	0.09**	0.22**	1.07	0.87	1.19	1.22	43.62
Number of kernel rows per ear	0.67**	1.39**	1.01	0.97	1.35	1.38	47.20
Number of kernels per row	2.31**	0.76**	0.40	6.03	4.63	0.76	73.82
100-Kernel weight (g)	1.42**	0.71**	0.50	3.99	2.84	0.71	78.17
Grain yield per plant (g)	19.88**	10.90**	0.52	6.34	39.76	10.90	70.75

*, ** Significant at 5 and 1 per cent probability levels, respectively.
*Heritability (NS) = Heritability Narrow Sense (Range: Low= <30%, Moderate= 30-60%, High= > 60

effects on earliness, grain yield, and various traits. Other commendable general combiners include HKI1332, HKI265, BML3 and HKI335, contributing valuable alleles to maize breeding. HKI295 is average, while BML3 excels in key traits. Utilizing these effective general combiners can enhance grain production and yield exceptional hybrids (Mosa *et al.*, 2021 and Ismail *et al.*, 2024).

Therefore, the parent alleles BPPT135, HKI1332, HKI265, BML3, and HKI335 that showed high or average gca effects for most characteristics might be widely used in repeated crossing programs to process favourable genes or create synthetic variations. These parents may be utilized directly to create exceptional single cross hybrids since they were the finest general combiners for numerous features with good performance.

There are 56 cross combinations affecting eleven agro-morphological variables in Table 4, but none have substantial SCA impacts. Still, some combinations worked. For every feature evaluated in the current study, not a single cross combination showed statistically significant sca effects in the intended direction at the same time. Nonetheless, it was noted that a number of cross combinations had notable and desired consequences for a wide range of attributes. Ten cross combinations showed a substantial to extremely significant sca influence on the number of days to 50% tasselling. Crosses HKI1332 X BML22, HKI1332 X BML3, BML6 X BML3, HKI586 X BML14, HKI586 X BML8, HKI295

X BML22, HKI295 X BML15, and HKI323-8 X HKI335 all had negative estimates of the sca impact and seemed to be good specific combiners for earliness. Seven cross combinations showed a substantial to extremely significant sca impact in the condition of days to 50% silking. A good combiner for earliness appeared to be the crosses BPPTI34 X HKI335, HKI1332 X BML3, BML6 X BML14, BML6 X BML8, HKI586 X BML22, HKI295 X BML22 and HKI323-8 X HKI335 that displayed negative estimations of the sca impact. Six cross combinations showed a substantial to extremely significant sca influence in Days to Maturity. The crosses between BPPTI34 and BML3, BPPT 135 and BML20, BPPT 135 and BML3, BPPT144 and BML14, BML6 and BML14 and HKI323-8 and HKI335 displayed negative estimations of the sca impact and seemed to be a suitable combiner of earliness. According to the calculations, there were substantial sca impacts for Plant Height in 13 out of 56 crossings. crosses BPPT135 X BML14, BPPT135 X BML8, BPPT144 X BML22, BPPT144 X BML20, BPPT144 X BML8, BML6 X BML22, BML6 X BML14, HKI586 X BML8, HKI586 X BML3, HKI586 X HKI335, and KI295 X BML15 were the good specific combiners of plant height that showed negative significant sca effects.

Twelve of the fifty-six cross combinations show a strong sca influence in the ear height trait, which was desired. As they demonstrate the tendency of ear height, the crosses BPPTI34 X BML15, BPPTI34 X BML3, BPPT144 X HKI335, HKI1332 X HKI335, BML6 X BML22, BML6 X BML20, BML6 X BML3, HKI586 X BML22, HKI586 X BML20, HKI586 X BML8, HKI295 X BML15 and HKI323-8 XBML14 showed a significant positive sca effect, indicating that they are good specific combiners. According to Kumara *et al*. (2013) and Chiuta *et al*. (2020) there is a beneficial sca impact in crosses of maize. Nine crosses show a strong positive sca impact for ear length, which is desired for this trait. A strong positive sca impact was shown by the crosses BPPTI34 X BML8, BPPT144 X BML14, HKI1332 X BML14, HKI1332 X HKI335, BML6 X BML22, HKI586 X BML20, HKI586 X BML15, HKI586 X BML3 and HKI295 X BML8. These crossings imply that they are good specific combiners of the trait. For ear grith 17 out of 56 cross combinations exhibits significant positive SCA effect. The crosses BPPTI34 X BML14, BPPT135 X BML20, BPPT135 X BML15, BPPT144 X BML15, BPPT144 X BML8, HKI1332 X BML14, HKI1332 X BML3, HKI1332 X HKI335, BML6 X BML20, BML6 X BML15, BML6 X BML14, HKI586 X BML22, HKI586 X BML15, HKI295 X BML22, HKI295 X BML15, HKI295 X BML8, HKI323-8 X BML8 were displayed significant desirable positive sca effect for ear girth.

In terms of the number of kernel rows per ear, 14 out of 56 cross pairings show a sizable sca effect, which is desired for this characteristic. A decent set of particular combiners were found for the crosses BPPTI34 X BML15, BPPT135 X BML14, BPPT144 X BML15, HKI1332 X BML14, HKI1332 X BML3, BML6 X BML22, BML6 X BML20, BML6 X BML3, BML6 X HKI335, HKI586 X BML15, HKI295 X BML8, HKI323-8 X BML15, HKI323-8 X BML14, HKI323-8 X HKI335. Out of all the crosses, only three showed the desired positive and substantial estimations of sca effects for the Number of Kernels per Row. As the best particular combiners, the crosses BPPTI34 X BML20, BPPT144 X HKI335, and HKI295 X BML3 were identified. This outcome is consistent with research by Keimeso *et al*. (2020), Ismail *et al*. (2022) and Shaaban *et al*. (2022). The remaining parent that had estimates of sca effects that were not statistically significant was categorized as an average or bad combiner. Significant estimates of the sca impacts were found for 16 crossovers for a 100-Kernel Weight. BPPT135 X BML14, BPPT135 X BML3, BPPT144 X BML22, BPPT144 X BML20, BPPT144 X HKI335, HKI1332 X BML20, HKI586 X BML15, HKI586 X HKI335, HKI295 X BML14, HKI295 X BML8, HKI295 X BML3, HKI323-8 X BML22 and HKI323-8 X HKI335 demonstrated a good specific combination. Desirable crosses are those with a positive and substantial sca impact for certain qualities. Other researches; Patel *et al*. (2019) and Nadeem *et al*. (2023) observed significant sca impacts in maize inbred lines for 100- kernel weight. Among the crosses, substantial and positive estimations of the sca impact were noted for grain yield per plant. There is a notable sca impact in eight cross pairings. HKI1332 X HKI335, HKI586 X BML14, BPPT135 X BML15, BPPT144 X BML22, BPPT144 X BML3, HKI295 X BML22, HKI295 X BML20 and HKI295 X BML8 were good examples of specialized combiners. The results of the present investigation are consistent with those of Ismail *et al*. (2019), Karim *et al*. (2022) and Lal *et al*. (2022), who found considerable to extremely significant levels of sca effects in the majority of the crosses they looked at for maize grain production.

The term “specific combining ability” (sca) refers to both epistatic interactions, which may be connected to heterosis, and non-additive genetic effects, which are mostly caused by dominance. It is challenging to address dominance and interaction effects. This may be taken

Table 4 : Estimates of SCA effects of hybrids (F_1) for eleven traits in maize.

S. no.	Crosses	50% DT	50% DS	DM	PH (cm)	EH (cm)	EL (cm)	EG (cm)	NKRE	NKPR	KW (g)	GYP (g)
1.	BPPTI34 X BML22	0.29	0.90	-1.46	8.82*	-4.30	-2.02**	0.15	-0.69	-2.08*	0.89*	-5.87*
2.	BPPTI34 X BML20	3.70**	-0.17	-0.09	-0.50	-0.83	0.37	-0.35*	0.44	1.89*	-1.02**	-1.89
3.	BPPTI34 X BML15	-4.75**	2.44	1.86	-4.79	12.25**	0.87	0.14	1.09**	-0.59	1.35**	3.76
4.	BPPTI34 X BML14	2.62**	0.48	4.60**	-9.31*	-4.86	0.48	0.39*	-0.88*	-0.06	0.87**	2.14
5.	BPPTI34 X BML8	0.95	0.53	0.74	3.39*	-1.61	1.79**	0.16	0.16	0.24	-0.31	1.11
6.	BPPTI34 X BML3	1.08	0.86	-4.63**	4.74	6.57*	-1.40*	-0.24	0.51	1.22	-0.86**	-3.71
7.	BPPTI34 X HKI335	-3.91**	-5.05**	1.03	-8.35*	-7.21*	0.65	0.04	-0.64	-0.62	-0.93**	4.45
8.	BPPT135 X BML22	-0.66	0.61	0.45	5.10	-4.37	-0.96	0.003	-0.74*	1.26	-0.50	-4.06
9.	BPPT135 X BML20	-1.24	-1.13	-3.57*	7.85*	-2.77	0.08	0.69**	0.06	0.65	0.43	2.31
10.	BPPT135 X BML15	2.29*	-1.17	-0.52	1.02	1.04	0.56	0.64**	0.57	0.56	-0.01	5.97*
11.	BPPT135 X BML14	0.67	2.20	4.52**	-8.43*	5.12	-0.46	-0.35*	2.33**	1.15	0.77*	-0.97
12.	BPPT135 X BML8	-1.32	-1.08	0.55	-10.08**	-3.09	-0.22	-0.23	-0.39	-1.19	-0.05	-3.34
13.	BPPT135 X BML3	-0.86	-1.08	-5.51**	2.50	1.66	0.01	0.27	-1.40**	-1.25	0.76**	0.72
14.	BPPT135 X HKI335	1.13	1.66	4.08**	2.03	2.40	0.98	0.25	-0.43	-1.17	-1.40**	-0.63
15.	BPPT144 X BML22	4.14**	4.61**	1.97	-22.48**	-11.82**	0.68	-0.09	-0.100	-2.25*	0.68*	5.94*
16.	BPPT144 X BML20	0.23	-0.13	0.07	-8.73*	-6.56*	-0.23	-0.06	0.104	-1.49	0.69*	0.39
17.	BPPT144 X BML15	-2.89	-1.50	-1.49	2.03	0.22	-0.18	0.33*	0.95**	-0.95	0.04	-1.08
18.	BPPT144 X BML14	-0.51	-1.46	-4.32**	21.67**	5.67	1.42*	-0.84**	-0.49	1.73	-1.10**	-7.83**
19.	BPPT144 X BML8	-0.51	-1.08	-0.41	-22.67**	-4.67	0.27	0.36*	-0.28	1.12	-0.22	-0.56
20.	BPPT144 X BML3	0.60	0.57	2.70	9.17*	-3.35	-1.33*	0.11	0.40	-0.97	0.09	4.83*
21.	BPPT144 X HKI335	-1.06	-1.00	1.47	21.01**	20.52**	-0.07	0.19	-0.58	2.81**	1.18**	-1.69
22.	HKI1332 X BML22	-2.66**	-1.95	-1.00	-1.99	-1.45	-0.68	0.30	-1.51**	-0.50	-0.11	-1.47
23.	HKI1332 X BML20	-0.91	-0.70	-0.66	-2.91	-4.45	-0.66	-0.74**	-0.64	-1.61	1.09**	-5.25*
24.	HKI1332 X BML15	3.96**	1.58	1.05	-3.10	0.39	-1.94**	-0.67**	-1.36**	0.02	-0.31	1.63
25.	HKI1332 X BML14	1.00	-0.13	-0.70	0.53	1.31	1.45**	0.57**	1.85**	0.45	-0.06	1.84
26.	HKI1332 X BML8	-0.99	0.33	0.33	6.75	-1.33	-0.70	-0.41*	0.16	-0.03	0.44	-2.35
27.	HKI1332 X BML3	-4.86**	-4.99**	-0.57	-0.48	0.38	0.63	0.47**	0.91**	1.07	-0.17	-1.91
28.	HKI1332 X HKI335	4.46**	5.75**	1.56	1.17	5.93*	1.89**	1.08**	0.59	0.59	-0.87**	7.52**
29.	BML6 X BML22	0.19	4.57**	3.50*	-14.25**	12.83**	2.37**	-0.28	0.94**	0.53	0.21	0.56
30.	BML6 X BML20	-1.38	2.15	3.41*	0.65	5.97*	-1.07	0.40*	0.91*	1.05	0.36	0.05
31.	BML6 X BML15	3.15**	0.44	0.67	2.56	-14.00**	0.34	0.37*	-0.13	0.39	0.27	-3.85
32.	BML6 X BML14	-0.13	-2.51*	-3.52*	-20.72**	-12.05**	-1.91**	0.45**	-2.78**	-0.94	-0.46	3.39
33.	BML6 X BML8	-0.80	-2.80*	-2.71	27.65**	1.35	-1.17*	-0.70**	-1.07**	-0.96	0.37	0.88

Table 4 continued....

34.	BML6 X BML3	-2.012*	-0.80	-1.79	-3.99	6.64*	0.46	-0.01	1.01**	-0.79	-0.21	-2.33
35.	BML6 X HKI335	0.98	-1.05	0.44	8.10*	-0.74	0.99	-0.23	1.12**	0.73	-0.11	1.30
36.	HKI586 X BML22	0.48	-7.42**	-0.69	29.46**	13.97**	-0.08	0.34*	0.06	1.73	-0.05	-0.36
37.	HKI586 X BML20	-1.43	-1.51	-1.52	-3.99	8.07**	1.36*	0.23	0.13	-0.58	-0.50	-1.18
38.	HKI586 X BML15	1.44	0.11	-1.76	17.08**	-9.55**	1.48**	0.70**	0.95**	1.22	0.67*	-0.15
39.	HKI586 X BML14	-5.85**	0.48	-2.22	17.42**	-3.72	0.25	0.29	-0.22	-1.68	-0.26	5.03*
40.	HKI586 X BML8	-1.85*	-0.47	-2.11	-37.99**	11.22**	-1.07	-0.33	-0.05	0.26	-0.56	-1.73
41.	HKI586 X BML3	3.94**	4.53**	4.37**	-10.84**	-12.98**	1.13*	-0.44**	0.20	-0.09	-1.07**	1.93
42.	HKI586 X HKI335	3.27**	4.28**	3.94**	-24.47**	-7.00**	-3.07**	-0.80**	-1.08**	-0.87	1.78**	-3.52
43.	HKI295 X BML22	-2.80**	-2.81*	-2.83	-4.54	-3.75	0.82	0.35*	1.90**	0.79	-0.60*	4.86*
44.	HKI295 X BML20	1.28	0.44	-0.12	-4.93	3.24	0.33	0.006	-0.95**	-0.22	-0.46	6.34**
45.	HKI295 X BML15	-6.17**	-1.60	0.16	-12.76**	14.70**	-0.07	0.40*	-0.40	-0.44	-0.74*	-3.96
46.	HKI295 X BML14	2.86**	2.77*	-0.72	1.01	-1.98	-1.23*	-0.50**	-1.35**	-0.68	0.87**	-4.98*
47.	HKI295 X BML8	2.53**	1.48	0.14	21.12**	-0.30	1.17*	0.33*	1.65**	0.03	0.74*	6.52**
48.	HKI295 X BML3	0.32	1.51	1.10	2.04	-3.81	-0.12	-0.07	0.37	2.20*	1.26**	-0.84
49.	HKI295 X HKI335	1.98*	1.23	2.27	0.08	-8.07**	-0.89	-0.52**	-1.21**	-1.67	-1.07**	-7.93**
50.	HKI323-8 X BML22	1.00	1.47	0.06	-0.10	-1.09	-0.13	0.13	0.13	0.52	1.29**	0.41
51.	HKI323-8 X BML20	-0.24	1.06	2.49	0.76	-2.66	0.58	-0.17	-0.05	0.31	-0.59*	-0.76
52.	HKI323-8 X BML15	2.96**	-0.31	0.02	-2.05	-4.27	-1.06	-0.64**	1.67**	-0.21	-1.28**	-2.31
53.	HKI323-8 XBML14	-0.66	-1.94	2.36	-0.14	10.50**	0.005	-0.02	1.54**	0.04	-0.62*	1.37
54.	HKI323-8 X BML8	2.00*	3.10*	3.46*	5.83	-1.54	0.48	0.81**	-0.17	0.53	-0.41	-0.52
55.	HKI323-8 X BML3	1.79*	2.43	4.32**	-3.18	4.87	0.61	-0.09	-2.02**	-1.39	0.19	1.31
56.	HKI323-8 X HKI335	-6.86**	-5.81**	-12.74**	0.42	-5.81*	-0.48	-0.01	2.25**	0.19	1.42**	0.51
C.D at 5%		1.79	2.48	2.86	7.15	5.67	1.09	0.33	1.09	1.85	0.56	4.66
SE (Sij)		0.90	1.25	1.44	3.61	2.86	0.55	0.16	0.55	0.93	0.28	2.35
SE (Sij – Skl)		1.28	1.77	2.04	5.10	4.05	0.78	0.23	0.78	1.32	0.40	3.32

*, ** Significant at 5 and 1 per cent probability levels, respectively.

advantage of by intercrossing and delaying selection until a later generation, thereby separating generations through a decrease in heterozygosity. It is crucial to identify hybrids that are appropriate for heterosis breeding as well as those that could be passed down for additional selection in successive generations of segregation. Highly significant sca effects of the crossings in hybrids show a substantial departure from what would have been expected given the performances of their parents (Chandel *et al*., 2019).

A careful examination of the results revealed that parents with different combinations of General Combining Ability (GCA) effects were included in crosses that showed notable and advantageous Specific Combining Ability (SCA) effects for different characteristics. Examples of good × good (G × G), good × average (G × A), average × average (A × A), average × poor (A × P), and poor × poor (P × P) GCA effects were included in these combinations. This finding emphasizes the lack of a clear relationship between the GCA effects that each parent exhibits for the variables under study and the positive and substantial SCA effects that are seen in crosses.

For every feature evaluated in the current study, not a single cross-combination showed statistically significant SCA effects in the intended direction at the same time. 8 out of the 56 crossings were determined to be good particular combiners for grain yield due to their positive and substantial sca effects, according to the estimations of sca effects, whereas the remaining 48 crosses were found to be average combiners. Given that they demonstrated the maximum desirable sca effect, the crosses BPPT135 X BML15, BPPT144 X BML22, BPPT144 X BML3, HKI1332 X HKI335, HKI586 X BML14, HKI295 X BML22, HKI295 X BML20 and HKI295 X BML8 can be designated as the best particular combiners for grain yield.

Among the 56 cross-combinations, none exhibited statistically significant SCA effects across all features. Only 8 combinations, such as BPPT135 X BML15 and HKI1332 X HKI335, displayed excellent grain yield potential. Notably, HKI295 X BML8 and HKI323-8 X HKI335 demonstrated optimal combinations for increased yields. Further exploration of these combinations holds promise for developing high-yielding, early maturing hybrids (Suhaisini *et al*., 2016; Rana *et al*., 2020 and Maphumulo *et al*., 2021).

The results of the current investigation indicated that, generally speaking, there was no correlation between the sca impacts of the single crosses and the parents' gca effects. Given that the mean performance of single crossings was highly dependent on the mean performance of the parents involved, the parents should be chosen using specific combing ability assessments. Therefore, as stated by Patel *et al*. (2022) and Nadeem *et al*. (2023), a high gca value of parents does not guarantee significant sca effects of their crosses.

The following conclusions are drawn from the study's findings: Because heterosis breeding is unfixable, which favours the creation of single cross hybrids, and because non-additive gene effects are more common than additive gene effects in the inheritance of yield and its component qualities, heterosis breeding would be more effective. A superior base population may also be produced by intercrossing the inbred lines that have favourable gca effects for grain production and other agro-morphological characteristics. Deriving elite lines that excel in desirable qualities would therefore become easier with further recurrent selection attempts. In terms of earliness, grain production per plant and component qualities, excellent single cross hybrids were discovered that either surpassed or equalled the criteria. Additionally, they demonstrated strong suppression of superior parents by a considerable margin, a big sca impact, and good per se performance. Therefore, in order to verify that these hybrids are appropriate for use in commerce, a thorough testing procedure may be applied to them in a range of temporal and geographical contexts (Patel *et al*., 2019 and Kamal *et al*., 2023).

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