Exploration of Diallel Method for Assessing Heterosis and Combining Ability in Maize (Zea mays L.)

ABSTRACT:

During the Kharif season of 2018 and Rabi season of 2018-19, an experimental study was conducted. The selection of seven maize genotypes was based on quantitative traits, growth duration, suitability for the Kharif season, and yield. These genotypes were then crossed in a half diallel mating design, resulting in the production of 21 single-cross hybrids. The cultivation of these hybrids, along with the seven parental inbred lines, totaling 28 genotypes, followed a randomized block design. Each plot had dimensions of 23.10m by 1.0m and maintained a plant density of 240 plants per plot. To assess the quantitative traits, observations were recorded from five randomly selected plants per plot. The analysis of variance indicated significant genetic variability among the genotypes, particularly in traits such as days to 50% germination, silking, maturity, plant height, number of leaves per plant, biological yield, cob ear weight, number of rows per cob, and number of seeds per cob. This variability was attributed to both additive and non-additive genetic components, as evident from significant variances due to general combining ability (GCA) and specific combining ability (SCA). The GCA/SCA ratio was less than unity for most traits. For most traits, parental lines P1, P2, and P4 exhibited high GCA effects. Additionally, F1 hybrids P4x P3, P3x P1, P5x P3, and P7 x P5 were found to be desirable in terms of yield and related traits. In terms of yield, seven crosses (P1 x P6, P2 x P7, P2x P5, P1 x P2, P3x P4, P5 x P7, and P3 x P5) outperformed the check hybrid, demonstrating their potential for future breeding programs aimed at enhancing maize yield.

Keywords: Maize, GCA, SCA, Heterosis, Combining Ability

1. INTRODUCTION:

Maize occupies the position of the third vital cereal crop in our nation, following rice and wheat, showcasing its versatile utility in the domains of food, animal feed, forage, and raw materials for industries. With its cultivation across diverse ecological landscapes in our country, our primary objectives revolve around the advancement of high-yielding hybrids that are resilient and adaptable to diseases, pests, and varying climate conditions. Simultaneously, we place significant emphasis on refining and enhancing our production systems. The primary goal for corn breeders is to explore the genetic resources in order to create novel varieties of maize with increased yield potential and superior quality. To achieve this, comprehending the distinct genetic components and their interactions across various environments, as well as the concept of heterosis for yield and its constituents, is crucial. The key to hybrid development in maize lies in identifying inbred lines, and the examination of combining ability plays a vital role, particularly in selecting potential parents for hybrid and synthetic development.

The essence of combining ability studies lies in their dependability, which offers crucial insights for selecting parents based on hybrid performance. It not only aids in understanding the nature of gene action for specific traits but also assists breeders in selecting diverse parents and optimal hybrid combinations. At the heart of this investigative framework lies the diallel analysis system, an extremely informative methodology. This approach enables us to estimate genetic parameters related to combining ability, uncovering the dominance relationships among the parents studied in the first filial generation, with or without reciprocals. Understanding the nature and extent of gene action through combining ability analysis is essential for designing effective breeding programs. The valuable information obtained from diallel analysis, widely used for estimating gene action types, can be summarized in two primary genetic parameters: General Combining Ability (GCA) and Specific Combining Ability (SCA). These parameters are crucial in formulating intelligent breeding strategies. The comprehension of the effects of General Combining Ability (GCA) and Specific Combining Abilities (SCA) serves as crucial benchmarks, determining the potential value of inbred lines in hybrid combinations.

In the intricate landscape of maize breeding, this research strives to navigate the complexities of combining ability analysis, utilizing the insightful diallel analysis system to unravel the genetic foundations governing the development of high-performance maize hybrids. The subsequent exploration of General Combining Ability(GCA) and Specific Combining Ability (SCA) in this context not only enhances our understanding of gene action but also establishes the basis for strategic advancements in hybrid breeding programs, poised to elevate the agricultural landscape.

2. MATERIALS AND METHOD:

The investigation was based on seven genotypes of Maize obtained from Chandra Shekhar Azad University, Kanpur (U.P). The selection of these types was based on their characteristics, duration, and suitability for the *Kharif* season, and yield potential. The seeds of the selected parental inbred lines were carefully planted in the experimental field. By using a half diallel crosses mating design, seven inbred lines were crossed systematically, resulting in the creation of 21 hybrid crosses during the *Kharif* season of 2018. In the following *Rabi* season of 2018-19, all 28 types, including the seven parental inbred lines and 21 F1 hybrids, were grown.

The cultivation design involved placing the seven parental inbred lines in a randomized block pattern, with each line having two plots. Each plot consisted of three replications, each 23.10m long, with a separation of 1.0m between them, ensuring a stand of 240 plants per replication. The arrangement of the types was structured with a 20 cm P x P distance, 45 cm L x L distance, and 60 cm G x G distance. The trials received comprehensive irrigation throughout the growth cycle, and cultural practices such as fertilization and weed control were carried out according to standard field protocols. Data collection included observations on 18 quantitative traits, collected from five randomly selected plants within each plot.

3. RESULTS AND DISCUSSION:

The effectiveness of selection procedures is crucial for determining the success of any breeding program. When dealing with polygenic traits that are greatly influenced by seasonal factors, such as those seen in maize, selecting the right traits becomes a difficult task. Most maize breeding programs aim to improve the potential yield, a complex trait that has been extensively studied. Grafius (1959) raised doubts about the presence of a single gene controlling yield and instead proposed a component breeding approach to enhance yield potential. Maize breeders need a thorough understanding of combining ability, gene actions, and inheritance patterns to identify the most suitable breeding methodology for their purposes, taking into account yield and its contributing factors.

Maize plants possess significant genetic variability in various characteristics, rendering them suitable for deliberate selection and hybridization to produce specific varieties or hybrids. In order to accomplish certain objectives in a breeding programme, it is crucial to conduct a carefully designed experiment to ascertain the patterns of inheritance of desired traits within the population. This study examines the combining ability, heterosis, heterobeltiosis, and economic heterosis of several yield and yield-related characteristics in maize. A half diallel mating technique is implemented, utilising genetically diverse parents cultivated in a randomized complete block design. The parents and their first-generation offspring are meticulously cultivated following a predetermined procedure, and the resulting data undergoes thorough statistical analysis to derive valuable insights.

The analysis of variance conducted on eighteen criteria divided the total variation into two components: the variation caused by genetics and the variation caused by other factors (Table 1). The variance analyses demonstrated substantial genetic variety among the genotypes for the assessed parameters, encompassing the duration for 50% germination, duration for 50% maturity, plant height, leaf count per plant, yield per plant, cob ear weight, and number of cob rows. The analysis revealed a substantial divergence among all the genetic varieties for the variables under investigation. The analysis of variance for yield and its component qualities for parents also indicated that the average sum of squares resulting from the duration needed for 50% germination and the duration needed for 50% silking were statistically significant. The statistical significance of the mean squared deviations was established for various variables including the time necessary for 50% maturity, plant height, leaf count per plant, yield per plant, cob ear weight, number of rows per cob, and number of seeds per cob, all of which were attributed to F1s. The statistical significance of the average sum of squares allocated to Parents compared to F1s was calculated for yield per plant. The results obtained in this study align with the findings of several previous studies, including those conducted by Murayam.m et al. (2003), Alam M.M.K.A. et al. (2008), S. Aliu et al. (2008), Amiruzzaman Mohammad et al. (2013), Badwy El.M. El. M. (2013), Rashmi K. et al. (2013), Albadawy Mahmoud (2013), Azad kalam abulmohammad et Al. (2014), Patel kumarmaulik (2015), ZelekeHabtamu (2015), AlamerewSentayehu and Warsi M.Z.K. (2015), Mahmood Sultan et al. (2016), ShenguKewetiMieso et al. (2016), Matin Islam Quamrul Mohammad et al. (2017), and Ola and Dubey (2017).

Table 1. Analysis of mean square values across various characters

SN	Characters	Source					
		Rep [2]	Genotype [27]	Parent [6]	F1 [20]	P vs F1 [1]	Error [54]
1	Days to 50% germination	0.57	3.66**	8.54**	2.37	0.32	1.35
2	Days to 50% tasseling	1.23	10.20	7.87	11.35	1.15	7.76
3	Days to 50% sillking	38.01	95.57	373.60**	4.64	246.04	95.67
4	Days to 50% maturity	15.37*	9.26**	6.33	10.32**	5.73	3.33
5	Plant height (cm)	547.68	1240.65**	284.94	1578.12**	225.35	461.00
6	No. of leaves per plant	0.81	1.49**	0.59	1.81**	0.50	0.40
7	Biological yield per plant (g)	25829.15**	6855.64**	4176.44	7374.94**	12544.78*	2163.98
8	No. of cobs per plant	0.08	0.05	0.02	0.06	0.04	0.05
9	Cob ear weight (g)	638.36	442.08*	164.97	509.37*	758.99	260.91
10	Cob length (cm)	8.88**	1.85	0.48	2.27	1.89	1.73
11	No. of rows per cob	1.71	2.39**	2.26	2.50**	0.86	1.06
12	No. of seed per row	19.19	8.54	5.92	9.61	2.95	11.54
13	No. of seed per cob	2818.27	3064.44	1860.59	3269.14*	6193.55	1838.94
14	100 Seed weight (g)	13.84	10.73	7.90	11.96	3.15	9.87
15	Shelling percent	27.28	102.48	91.72	110.52	6.15	113.16
16	Harvesting index (%)	60.62	22.61	35.38	19.35	11.12	23.88
17	Seed yield per cob (g)	195.87	173.96	132.46	182.43	253.48	145.38
18	Seed yield Per Plant (g)	88.65	211.93	248.84	196.33	302.33	207.01

[] Degrees of freedom
*, ** Significant at 5% and 1% respectively

In order to effectively maintain the current genetic diversity, it is essential to possess a thorough comprehension of the genetic control of traits. The breeder's choice of the most appropriate breeding strategy is mostly based on the behaviour of combining ability and the sort of gene action that controls the features of interest. The genetic mechanism linked to yield and its constituent characteristics plays a crucial role in determining the effectiveness of breeding methods. General combining ability is defined by the presence of additive, additive x additive, and higher levels of additive x additive interaction, and it demonstrates stability. In contrast, specialized combining ability is associated with non-additive gene activity, such as dominance, dominance x dominance, and additive x dominance, and it does not possess stability. Significant advancements can be achieved using traditional breeding procedures when the impact of general combining ability is more prominent. Nevertheless, when dealing with traits that exhibit significant non-additive gene effects, employing a recurrent selection method like diallel selective mating or bi-parental selective mating during the initial generations can be a highly productive breeding technique.

The analysis of variance for combining ability in grain yield and its components showed that the variance attributed to general combining ability (GCA) was statistically significant for various traits, such as time taken for 50% germination, plant height, number of leaves per plant, biological yield per plant, weight of cob ear, number of rows per cob, and 100-seed weight. In contrast, the mean square sum attributable to SCA was found to be statistically significant for variables such as days to maturity, plant height, number of leaves per plant, biological yield per plant, number of rows per cob, and number of seeds per cob. The significant disparity ascribed to both General Combining Ability (GCA) and Specific Combining Ability (SCA) suggests that both additive and non-additive factors play a crucial role in the inheritance of these traits (Table 2). For all parameters, except the number of cobs per plant and seed output per cob, the ratio of changes ascribed to general combining ability (GCA) and specific combining ability (SCA) was less than one. These findings indicate that non-additive factors have a more prominent role in the inheritance of these particular characteristics. The results obtained in this study are consistent with the findings of several previous studies, including those conducted by Murayam.m et al. (2003), Alam M.M.K.A. et al. (2008), S. Aliu et al. (2008), Amiruzzaman Mohammad et al. (2013), Badwy El.M. El. M. (2013), Rashmi K. et al. (2013), Albadawy Mahmoud (2013), Azad kalam abulmo hammad et al. (2014), Patel kumarmaulik (2015), ZelekeHabtamu (2015), AlamerewSentayehu and Warsi M.Z.K. (2015), Mahmood Sultan et al. (2016), ShenguKewetiMieso et al. (2016), Matin Islam Quamrul Mohammad et al. (2017), and Ola and Dubey (2017).

Table 2. Comparative evaluation of combining ability mean squares and error mean squares across diverse traits

SN	Characters	Source			Var Model I	
		GCA [6]	SCA [21]	Error [54]	GCA	SCA
1	Days to 50% germination	3.13**	0.68	0.45	1.78	4.77
2	Days to 50% tasseling	1.62	3.91	2.59	-0.64	27.77
3	Days to 50% sillking	54.31	25.44	31.89	14.95	-135.40
4	Days to 50% maturity	2.35	3.30**	1.11	0.83	45.95
5	Plant height (cm)	554.96**	373.14**	153.67	267.53	4609.02
6	No. of leaves per plant	0.80**	0.41**	0.13	0.44	5.85
7	Biological yield per plant (g)	1709.24*	2449.78**	721.33	658.61	36297.47
8	No. of cobs per plant	0.02	0.02	0.02	0.00	-0.00
9	Cob ear weight (g)	222.92*	125.77	86.97	90.64	814.86
10	Cob length (cm)	0.54	0.64	0.58	-0.02	1.34
11	No. of rows per cob	0.94*	0.76*	0.35	0.39	8.50

12	No. of seed per row	3.31	2.72	3.85	-0.36	-23.72
13	No. of seed per cob	596.20	1142.99*	612.98	-11.19	11130.11
14	100 Seed weight (g)	8.26*	2.24	3.29	3.31	-22.08
15	Shelling percent	24.88	36.81	37.72	-8.56	-19.07
16	Harvesting index (%)	11.64	6.36	7.96	2.45	-33.53
17	Seed yield per cob (g)	94.13	47.66	48.46	30.45	-16.79
18	Seed yield Per Plant (g)	87.80	65.74	69.00	12.53	-68.51

[] Degrees of freedom
*, ** Significant at 5% and 1% respectively.

The nature and extent of combining ability effects provide insights into the relative influence of fixable and non-fixable gene effects in the inheritance of various traits. Consequently, it aids in the identification of suitable parent plants for the crossing program.

The traditional approach of choosing parents based on individual performance and local adaption may not necessarily produce substantial outcomes. The reason for this is that the efficacy of parental contribution relies on the intricate interplay between genes and the genotype-environment interface. The GCA estimates of parent P1 (-0.48*) and parent P5 (-0.51*) revealed favorable results for days to 50% germination in this investigation. The genetic cross analysis (GCA) demonstrated a significant and positive impact on the time taken for 50% silking in parent P2, with a decrease of -5.52**. Parent P3 (-0.82*) shown favorable general combining ability (GCA) effects for the trait of days to 50% maturity. Therefore, parents exhibiting negative general combining ability (GCA) effects were regarded as favorable contributors for this particular feature. Within the group of parents, the genetic combining ability (GCA) had positive effects on the number of leaves per plant in parent P4 (0.57*). In addition, the GCA impacts were similarly favorable for the biological yield per plant (g) in parent P4 (19.63*). Parent P1 (5.91*) had favorable general combining ability (GCA) effects on Cob ear weight. Parent P4 demonstrated positive general combining ability (GCA) impacts for the number of rows per cob. Both parents, P1 (1.13*) and P2 (1.28*), showed statistically significant positive general combining ability (GCA) effects for 100-seed weight. Parent P1 exhibited notable and statistically significant general combining ability (GCA) effects (4.63*) on seed yield per cob, as well as positive and statistically significant GCA effects (5.24*) on seed yield per plant. Therefore, parent plants P1, P2, and P4 were recognized as having substantial General Combining Ability (GCA) effects and were deemed excellent general combiners for yield and its contributing qualities (Table 3-4).

Overall, it was noted that the parents who performed the best individually also showed significant effects in terms of their ability to combine well with other parents. Due to the additive x additive gene effects, the parents in question have a favorable genetic position for the qualities in question. This makes them suitable for use in a multiple crossing program, which can result in a population with a greater accumulation of desirable genes (Griffing, 1956a).

Table 3. Analysis of general and specific combining ability effects on key agronomic traits

SN	Genotype	Days to 50% germination	Days to 50% tasseling	Days to 50% sillking	Days to 50% maturity	Plant height (cm)	No. of leaves per plant	Biological yield per plant (g)	No. of cobs per plant	Cob ear weight (g)
1	P1	-0.48*	-0.79	1.07	-0.01	3.50	-0.14	10.89	-0.01	5.91*
2	P2	-0.14	0.35	-5.52**	-0.45	0.05	-0.11	3.22	-0.01	5.06
3	P3	0.75**	0.10	1.59	-0.82*	5.45	0.12	1.78	-0.08*	-4.45
4	P4	0.93**	-0.35	0.81	0.11	4.22	0.57**	19.63*	-0.02	0.69
5	P5	-0.51*	0.35	0.78	0.44	4.33	-0.08	-1.33	0.06	3.15
6	P6	-0.29	0.24	0.59	0.70*	-0.48	0.03	-12.85	0.01	-6.60*
7	P7	-0.25	0.10	0.67	0.03	-17.07**	-0.39**	-21.33*	0.06	-3.77
8	P2 x P1	-0.08	0.38	7.86	-2.09*	5.82	0.23	85.39**	0.11	11.08
9	P3 x P1	-0.64	-0.36	0.08	1.94*	15.34	-0.13	16.50	0.05	13.72
10	P4 x P1	-0.16	-0.58	-1.14	-1.31	12.78	0.61	-9.35	0.05	8.03
11	P5 x P1	0.95	-2.29	-0.44	-1.65	-7.66	0.13	17.61	-0.09	9.25
12	P6 x P1	-0.60	-1.18	-1.92	-0.57	3.54	-0.39	-4.54	-0.11	-3.72
13	P7 x P1	0.03	-1.03	-1.66	1.43	-14.54	-1.09**	-27.72	-0.22	-0.64
14	P3 x P2	0.03	1.16	6.01	0.06	-13.33	-0.69*	-15.17	-0.08	-4.01
15	P4 x P2	-0.49	1.94	6.12	0.13	19.84	0.59	36.31	-0.15	15.17
16	P5 x P2	-0.05	0.56	6.16	1.13	0.33	-0.43	-16.72	0.04	-5.98
17	P6 x P2	0.73	-1.99	4.34	2.87**	-21.13	-0.81*	-65.54**	0.02	-11.53
18	P7 x P2	-0.64	0.16	3.94	-0.80	21.92	0.82*	39.61	-0.02	-2.51
19	P4 x P3	-0.71	-1.47	-1.32	0.17	27.10*	0.90**	80.09**	-0.08	-6.99
20	P5 x P3	-0.94	3.16*	-1.29	-1.83	13.72	1.01**	14.39	-0.02	3.46
21	P6 x P3	1.18	-0.06	0.23	-4.43**	-1.14	-0.44	-63.43*	-0.04	-4.75
22	P7 x P3	-0.53	-1.92	-0.18	-1.43	-14.09	-0.27	-36.94	0.18	-14.36
23	P5 x P4	1.21*	-0.73	-2.18	-0.09	-0.84	-0.44	6.87	-0.02	-1.96
24	P6 x P4	-0.01	1.05	-1.32	0.98	8.10	0.44	15.72	0.09	1.82
25	P7 x P4	-0.71	3.19*	0.27	1.65	-49.32**	-0.46	0.54	0.12	-0.01
26	P6 x P5	0.44	0.01	-0.95	-0.35	-14.68	0.42	-13.65	0.15	-3.37
27	P7 x P5	-0.94	3.49*	-2.36	-0.35	30.24**	0.52	89.17**	0.24*	24.82**
28	P7 x P6	1.18	-2.06	0.49	1.39	-2.15	0.41	-0.98	0.02	8.92
	Standard error									
	Gi	0.21	0.50	1.74	0.33	3.83	0.11	8.29	0.04	2.88
	Gi-Gj	0.32	0.76	2.66	0.50	5.84	0.17	12.66	0.06	4.40
	Sii	0.51	1.23	4.31	0.80	9.47	0.28	20.51	0.10	7.12
	Sij	0.60	1.44	5.07	0.95	11.13	0.33	24.11	0.11	8.37
	Sij-ik	0.89	2.14	7.53	1.41	16.53	0.49	35.81	0.17	12.43
	Sij-Skl	0.84	2.01	7.04	1.31	15.46	0.46	33.50	0.16	11.63

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

Table 4. Evaluation of General and Specific Combining Ability Effects on Cob Characteristics and Yield Metrics

SN	Genotype	Cob length (cm)	No. of rows per cob	No. of seed per row	No. of seed per cob	100 Seed weight (g)	Shelling percent	Harvesting index (%)	Seed yield per cob (g)	Seed yield Per Plant (g)
1	P1	-0.07	-0.11	1.13	13.94	1.13*	2.75	1.66	4.63*	5.24*
2	P2	0.44	-0.11	-0.34	-0.26	1.28*	-0.46	0.43	1.87	1.02
3	P3	-0.27	-0.47*	-0.39	-3.96	-0.98	-0.97	-1.05	-3.01	-4.69
4	P4	-0.04	0.42*	0.22	3.56	-0.30	-1.00	-1.83*	-0.00	-0.61
5	P5	0.12	0.29	0.37	4.21	0.46	1.27	-0.00	2.90	1.73
6	P6	-0.26	-0.25	-0.52	-10.13	-0.62	0.61	0.56	-3.19	-2.08
7	P7	0.07	0.23	-0.47	-7.37	-0.97	-2.21	0.23	-3.19	-0.60
8	P2 x P1	-0.50	-0.69	-0.66	-4.79	0.91	4.15	-3.82	-1.69	1.56
9	P3 x P1	1.86**	-0.15	1.34	30.17	3.37*	5.49	1.64	13.62*	11.54
10	P4 x P1	-0.06	-0.02	-0.02	9.81	-0.32	-9.34	-0.28	-0.97	-0.53
11	P5 x P1	-0.22	0.15	0.19	-23.13	-0.60	-9.39	-1.36	-0.43	1.01
12	P6 x P1	-0.05	0.34	-1.56	4.56	0.67	4.73	-0.93	2.93	-4.15
13	P7 x P1	-0.03	0.40	1.03	22.32	0.07	4.62	1.01	4.58	-4.24
14	P3 x P2	-0.58	0.37	-0.78	-0.48	-1.24	-1.80	-1.63	-2.48	-5.55
15	P4 x P2	1.37*	-0.00	-0.84	-6.03	2.21	-6.02	-0.36	4.97	0.82
16	P5 x P2	-0.27	-0.64	0.86	12.06	-0.62	0.64	-0.09	-1.02	-4.62
17	P6 x P2	0.54	-0.05	-0.25	-0.42	-1.32	3.43	0.97	-3.38	-1.82
18	P7 x P2	1.09	-0.28	-0.42	-35.56	1.04	-5.35	-3.67	-5.05	-6.68
19	P4 x P3	0.54	-0.04	-2.42	-18.94	-1.54	0.13	-4.67	-4.84	-8.16
20	P5 x P3	0.18	1.90**	3.44	62.59**	-0.61	10.84	2.41	8.97	9.33
21	P6 x P3	-0.51	-0.20	-1.45	-37.46	1.62	-2.25	2.74	-4.66	-3.08
22	P7 x P3	-1.28	0.11	-0.68	-35.27	-0.57	-0.98	1.31	-8.93	2.10
23	P5 x P4	-0.80	-0.09	-0.75	-0.72	0.35	1.89	0.77	0.68	0.94
24	P6 x P4	-0.58	0.39	3.31	31.18	-0.41	8.78	1.71	7.01	14.07
25	P7 x P4	-0.34	0.58	2.73	54.96*	-2.78	4.46	1.47	2.96	7.96
26	P6 x P5	-0.14	-2.08**	-1.57	-42.26	0.32	-10.14	-4.45	-9.54	-9.76
27	P7 x P5	0.88	1.51**	0.34	39.85	1.98	-3.58	2.74	11.01	15.66*
28	P7 x P6	0.71	-0.29	0.41	41.65	-0.17	2.96	0.07	7.33	6.58
	Standard error									
	Gi	0.23	0.18	0.61	7.64	0.56	1.90	0.87	2.15	2.56
	Gi-Gj	0.36	0.28	0.92	11.67	0.86	2.90	1.33	3.28	3.92
	Sii	0.58	0.45	1.50	18.91	1.39	4.69	2.15	5.32	6.34
	Sij	0.68	0.53	1.76	22.22	1.63	5.51	2.53	6.25	7.46
	Sij-ik	1.01	0.79	2.61	33.01	2.42	8.19	3.76	9.28	11.08
	Sij-Skl	0.95	0.74	2.45	30.88	2.26	7.66	3.52	8.68	10.36

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

Out of the 21 pairings, unfavorable SCA impacts were detected for Days to 50% maturity in two instances. The combinations were P2 multiplied by P1, resulting in -2.09*, and P6 multiplied by P3, resulting in -4.43**. Two combinations, P4 x P3 and P7 x P5, had considerable favorable effects on plant height, with increases of 27.10* and 30.24** respectively. In addition, three combinations demonstrated significant positive specific combining ability (SCA) impacts for the number of leaves per plant. The combinations consisted of P7 multiplied by P2 (0.82*), P4 multiplied by P3 (0.90**), and P5 multiplied by P3 (1.01**). Likewise, three combinations exhibited notable favorable benefits on the biological yield per plant. The combinations observed were P3 multiplied by P1 (85.39**), P4 multiplied by P3 (80.09**), and P7 multiplied by P5 (89.17**). A particular combination, namely P7x P5 (0.24*), shown a noteworthy increase in the sac effects on the number of cobs per plant. A different combination, specifically P7x P5 (24.82**), shown a notable increase in sac effects for Cob ear weight. Furthermore, two combinations, P3x P1 (with a statistically significant effect of 1.86**) and P4x P2 (with a statistically significant effect of 1.37*), demonstrated a beneficial impact on Cob length. Similarly, two combinations, P5x P3 (1.90**) and P7x P5 (1.51*), exhibited notable and statistically significant positive impacts on the number of rows per cob. In addition, two combinations, P5x P3 (62.59**) and P7x P4 (54.96*), exhibited statistically significant favorable effects on the number of seeds per row. The cross combination P3x P1 (3.37*) showed a notable increase in the sac effects for the weight of 100 seeds. Furthermore, P3x P1 (13.62*) exhibited a noteworthy increase in sac impacts for Seed yield per cob. Furthermore, a specific combination, P7x P5 (15.66*), shown a notable and statistically significant increase in the sac impacts on seed output per plant. Among the 21 combinations, 10 combinations showed no significant positive effects on the seed output per plant.

Therefore, to summarize, crosses such as P4x P3, P3x P1, P5x P3, and P7 x P5 exhibited strong SCA effects, which had a noteworthy influence on the seed yield per plant and its contributing attributes.

The effective utilization of heterosis in maize is mostly contingent upon the substantial impact of specific combining ability (SCA) effects (Tyagi et al., 2010). A cross combination that shows significant specific combining ability (SCA) effects and involves at least one parent with strong general combining ability (GCA) for a particular trait has the potential to create desirable transgressive segregants in future generations (Jinks and Jones, 1958). Nevertheless, it is important to acknowledge that while there may be significant impacts of specific combining ability (SCA) in crosses, these effects may not necessarily align with the general combining ability (GCA) effects observed in the parents. This suggests that inter allelic interactions pertaining to the trait under consideration play a crucial role.

The study investigated the impact of special combining ability (SCA) on various cross combinations. The findings demonstrated a notable and favourable influence of SCA on crop production and its constituent characteristics. The crossovers were generated as a result of crossing parents with differing levels of genetic combining ability (GCA). The crossings included parents with contrasting levels of general combining ability (GCA), namely good x poor GCA, poor x poor GCA, and poor x good GCA. These crosses illustrate several types of gene interactions, such as additive x dominance, additive x dominance, dominance x dominance, and dominance x additive, respectively.

Overall, the results showed that P1, P2, and P4 were the most favourable parents because they had strong general combining ability (GCA) effects on most of the traits. The F1 crosses P4x P3, P3x P1, P5x P3, and P7 x P5 exhibited favourable yield and yield-contributing characteristics.

The exploitation of heterosis in crop improvement has been extensively studied and applied by plant breeders. However, the effectiveness of hybrid vigor in enhancing crop output depends on the degree of heterosis and the practicality of producing hybrid seeds on a large scale. The magnitude of heterosis is mostly determined by non-adaptive gene action and the extensive genetic variation across parental plants. Mackey (1976) suggests that the superiority of hybrids compared to their superior parents can be ascribed to dominance, overdominance, or a mix of both. In breeding operations, the assessment of the superiority of F1 hybrids is conducted by comparing them to the mid parent, superior parent, or standard check. This evaluation is done to identify their suitability for commercial utilization of heterosis. The analysis revealed that the parent vs. crosses component of variation had a statistically significant impact on the biological yield per plant. The aim of this study on heterosis was to determine the most advantageous cross combination.

The heterosis range was determined to be wider than that of the standard check for majority of the characteristics. The results are consistent with prior research undertaken by Welcker C. et al. (2004), Gissa W.D. et al. (2007), Dhillon B.S. and Singh J. (2007), Amiruzzaman Mohammad et al. (2013), AlamerewSentayehu and Warsi M.Z.K. (2015), and Khan Ruhana and Dubey B. (2015).Analysis of heterosis for various traits revealed that out of the twenty-eight crosses, the combinations P1 x P6, P2 x P7, P2 x P5, P1 x P2, P3 x P4, P5 x P7, and P3 x P5 exhibited the most significant heterotic effects in the intended direction for yield attributes.The current study's heterosis estimates provide evidence for the profitable utilisation of heterosis in ridge gourds, as they demonstrate significant levels of heterobeltiosis and standard heterosis for yield and its various components. The crosses P1 x P6, P2 x P7, P2 x P5, P1 x P2, P3 x P4, P5 x P7, and P3 x P5 exhibited significant specific combining ability (SCA) effects for yield-related traits, along with strong individual performance and heterotic effects. Therefore, these crosses are suitable for the commercial utilisation of heterosis for certain characteristics.

The check hybrid was outperformed by the following seven crosses: P1 x P6, P2 x P7, P2 x P5, P1 x P2, P3 x P4, P5 x P7, and P3 x P5. The crosses exhibit exceptional performance individually, making them suitable for potential utilisation in future breeding programmes to generate yield segregants (Table 5-10).

Seven crossings (P1 x P6, P2 x P7, P2 x P5, P1 x P2, P3 x P4, P5 x P7, and P3 x P5) out-yielded the check hybrid. Because these crosses perform well on their own, future breeding projects may take use of them to create fruit yield segregants (Table 5-10). Crosses involving good x good general combiners, high SCA effects, and high per se performance may provide a high frequency of transgressive segregants. A straightforward pedigree procedure could be used to separate this cross. For crosses combining good x poor or poor x poor general combiners, biparental mating or diallel selective mating (Jensen 1970) and a recurrent selection technique are required.

Table 5. Exploring the extent of heterosis on days to 50% germination, days to 50% tasseling and days to 50% sillking

SN.	Crosses	Days to 50% germination			Days to 50% tasseling			Days to 50% sillking		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-3.45		-15.15	-0.41			21.15*		
2.	P1 x P3	-10.77		-12.12	-1.85	-1.24		1.74		
3.	P1 x P4	-4.62		-6.06	-1.25			-0.35		
4.	P1 x P5	11.11		-9.09	-3.11	-1.68		-0.00		
5.	P1 x P6	-0.00		-21.21*	-4.24	-3.27		-1.05	-1.05	
6.	P1 x P7	-5.08		-15.15	-2.27	-1.25		-0.87	-0.70	
7.	P2 x P3	-4.48		-3.03	2.28			19.02*		
8.	P2 x P4	-7.46		-6.06	4.20			18.20*		
9.	P2 x P5	0.00		-15.15	2.71			17.72*		
10.	P2 x P6	14.81		-6.06	-3.05	-1.24		16.22		
11.	P2 x P7	-11.48	-10.00	-18.18*	1.46			15.57		
12.	P3 x P4	-10.81	-10.81	0.00	-0.63			-0.35	-0.35	
13.	P3 x P5	-11.11		-15.15	5.42*			-0.69	-0.35	
14.	P3 x P6	14.75			-1.22			1.39		
15.	P3 x P7	-11.76	-3.23	-9.09	-1.66	-1.25		0.87		
16.	P4 x P5	11.11			1.48			-2.41	-2.08	
17.	P4 x P6	4.92		-3.03	1.03			-1.04	-0.70	
18.	P4 x P7	-11.76	-3.23	-9.09	5.68*			0.52		
19.	P5 x P6	16.00		-12.12	0.00			-1.04	-0.35	
20.	P5 x P7	-12.28	-3.85	-24.24**	6.28*			-2.59	-2.08	
21.	P6 x P7	16.36		-3.03	-3.27	-1.25		0.87		

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

Table 6. Exploring the extent of heterosis on Days to 50% maturity, Plant height (cm) and No. of leaves per plant

SN.	Crosses	Days to 50% maturity			Plant height (cm)			No. of leaves per plant		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-1.86	-0.80		7.26	5.49	12.05	0.00		
2.	P1 x P3	0.00	0.00		14.41	13.70	20.76*	-1.96		
3.	P1 x P4	-1.19	-0.53		11.54	11.47	18.55	8.39	7.01	6.33
4.	P1 x P5	-2.35*	-1.84		0.79	0.44	6.68	2.72		
5.	P1 x P6	-0.92	-0.79		0.26		10.42	-6.15		
6.	P1 x P7	1.06			-10.28			-12.93**		
7.	P2 x P3	-0.80			-1.72		2.01	-6.58		
8.	P2 x P4	0.67			15.42	13.44	20.65*	9.09*	7.01	6.33
9.	P2 x P5	0.53			5.03	3.65	9.33	-2.05		

10.	P2 x P6	2.52*			-13.27			-9.45*		
11.	P2 x P7	0.00			10.81	6.55	9.44	7.53	3.97	
12.	P3 x P4	-0.66	-0.00		21.23*	20.40*	28.04**	13.55**	12.10*	11.39*
13.	P3 x P5	-3.13**	-2.62*		14.37	14.05	20.30*	14.29**	9.80	6.33
14.	P3 x P6	-4.59**	-4.46**	-0.55	-0.59		8.82	-4.21		
15.	P3 x P7	-1.85	-1.07		-8.28			-2.04		
16.	P4 x P5	-0.39			4.88	4.44	11.08	2.68		
17.	P4 x P6	1.06			2.99		13.49	7.35	7.01	6.33
18.	P4 x P7	2.00			-30.10**			-0.67		
19.	P5 x P6	-0.91	-0.52		-8.65		0.26	6.40	1.28	
20.	P5 x P7	-0.53			16.63	10.73	16.80	8.51	8.51	
21.	P6 x P7	1.45			-8.94			3.03		

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

Table 7. Exploring the extent of heterosis on biological yield per plant (g), no. of cobs per plant and cob ear weight (g)

SN.	Crosses	Biological yield per plant (g)			No. of cobs per plant			Cob ear weight (g)		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	42.77**	40.70**	64.38**	2.70	0.00		25.46	14.36	11.48
2.	P1 x P3	11.68	7.53	35.72*	0.00			25.87	22.23	4.10
3.	P1 x P4	15.11	13.37	32.46*	0.00			28.68	28.35	3.52
4.	P1 x P5	22.82	15.47	34.90*	-5.56			33.74*	33.54	7.47
5.	P1 x P6	-5.76		21.18	-11.11			3.42	3.31	
6.	P1 x P7	2.97		8.28	-16.67			18.25	11.44	
7.	P2 x P3	-0.11		19.69	-9.09			-7.87		
8.	P2 x P4	30.50*	30.42*	47.95**	-14.29			23.80	13.11	10.26
9.	P2 x P5	8.92	3.83	17.79	8.57	5.56		1.36		
10.	P2 x P6	-26.55*			2.86			-17.08		
11.	P2 x P7	28.17*	16.89	32.59*	2.86			2.67		
12.	P3 x P4	37.95**	30.89*	65.20**	-6.25			-8.03		
13.	P3 x P5	13.40	2.91	29.88	6.25	0.00		8.81	5.81	
14.	P3 x P6	-29.87**			-0.00			-14.45		
15.	P3 x P7	-8.23		0.80	25.00	17.65		-18.62		
16.	P4 x P5	24.07	18.35	34.09*	5.88	5.88		11.48	11.36	
17.	P4 x P6	4.87		33.00*	11.76	11.76		3.57	3.40	
18.	P4 x P7	19.32	8.87	23.36	17.65	17.65		11.43	4.75	
19.	P5 x P6	-7.49		12.49	23.53	23.53		0.04		
20.	P5 x P7	53.77**	46.76**	50.93**	35.29*	35.29*		50.26**	41.40*	13.80
21.	P6 x	-6.33		9.50	11.76	11.76		13.93	7.26	

P7

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

Table 8. Exploring the extent of heterosis on cob length (cm), no. Of rows per cob and no. of seed per row

SN.	Crosses	Cob length (cm)			No. of rows per cob			No. of seed per row		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	0.79		0.71	-7.81		0.68	-4.76		
2.	P1 x P3	10.40*	10.40*	8.49	3.01		2.10	5.65		7.95
3.	P1 x P4	1.03		0.47	1.56		10.92	2.50		4.58
4.	P1 x P5	-0.31		0.47	2.69	0.90	11.21	3.99		6.23
5.	P1 x P6	0.96	0.64		-0.92		8.28	-7.75		
6.	P1 x P7	2.31	1.66	1.18	7.41	6.04	12.80	9.09		6.23
7.	P2 x P3	-0.55			4.57		6.63	-6.56		
8.	P2 x P4	8.48	7.97	9.67	-0.89		11.06	-3.90		
9.	P2 x P5	0.23		2.67	-5.95		4.52	4.45	2.40	2.63
10.	P2 x P6	4.47	3.10	4.72	-6.40		4.95	-4.77		
11.	P2 x P7	8.29	7.20	8.88	-0.73		7.08	-0.40		
12.	P3 x P4	2.92	1.72	2.36	5.58		7.65	-9.59		
13.	P3 x P5	0.62		1.42	21.80**	11.66	23.07**	18.41	18.38	14.03
14.	P3 x P6	-2.23			-1.46		0.54	-8.72		
15.	P3 x P7	-4.61			9.67	3.43	7.22	0.16		
16.	P4 x P5	-4.01			2.37	1.52	13.77	1.82	1.68	
17.	P4 x P6	-2.60			0.95	0.89	13.20	16.52	16.25	12.15
18.	P4 x P7	-0.24			10.22	6.09	18.89**	20.15	14.33	9.78
19.	P5 x P6	-1.09		0.00	-18.16**			-5.66		
20.	P5 x P7	4.88	2.97	6.37	17.55**	14.06*	25.71**	8.99	3.58	
21.	P6 x P7	4.60	4.27	3.77	-1.98		5.80	4.83		

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

Table 9. Exploring the extent of heterosis on no. of seed per cob, 100 seed weight (g) and shelling percent

SN.	Crosses	No. of seed per cob			100 Seed weight (g)			Shelling percent		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-1.54		1.39	9.78	5.41	15.79	4.52	1.57	27.13
2.	P1 x P3	16.79	12.86	14.21	23.20*	15.44	16.72	13.71	2.81	28.67
3.	P1 x P4	16.23	7.66	8.94	0.36		2.46	-14.45		1.30
4.	P1 x P5	-0.55			2.90	2.20	4.75	-17.05		5.37
5.	P1 x P6	5.83		1.18	9.11	4.51	5.66	10.43	4.00	30.17
6.	P1 x P7	25.34	8.29	9.59	4.81	0.03	1.14	8.35		24.78
7.	P2 x P3	-3.76			-3.54			-0.30		9.31
8.	P2 x P4	1.17			8.16	4.82	15.14	-11.67		1.47
9.	P2 x P5	6.42		4.31	-0.76		5.36	-4.53		17.92
10.	P2 x P6	-4.17			-4.18			6.55	3.16	21.84
11.	P2 x P7	-10.28			5.54		6.45	-10.00		0.48
12.	P3 x P4	-0.55			-9.41			5.14	0.20	11.89
13.	P3 x P5	33.05*	30.87*	23.51	-0.75			18.03	5.33	35.78*
14.	P3 x P6	-16.89			10.72	8.21	0.17	4.33		10.46
15.	P3 x P7	-6.40			-2.21			4.31	2.32	7.61
16.	P4 x P5	13.37	10.25	0.64	-0.31		2.46	-0.87		19.24
17.	P4 x P6	22.36	19.81	7.84	-4.13			17.63	17.07	30.72
18.	P4 x P7	48.46**	37.62*	18.71	-17.02			8.44	5.29	17.57
19.	P5 x P6	-13.95			3.37		0.82	-16.45		0.05
20.	P5 x P7	36.75*	23.56	12.78	10.10	4.40	7.00	-8.63		6.94
21.	P6 x P7	31.54*	19.60	7.65	-0.53			9.17	6.50	17.77

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

Table 10. Exploring the extent of heterosis on harvesting index (%), seed yield per cob (g) and seed yield per plant (g)

SN.	Crosses	Harvesting index (%)			Seed yield per cob (g)			Seed yield Per Plant (g)		
		Het	Hb	EH	Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-29.41*			1.21		18.37	-1.85		19.71
2.	P1 x P3	5.98			39.32*	29.57	40.67	26.74	6.58	27.70
3.	P1 x P4	-7.98			12.43	6.72	15.87	8.16		12.73
4.	P1 x P5	-10.96			12.71	11.92	23.24	9.31	0.17	20.02
5.	P1 x P6	-8.59			15.49	8.14	17.40	-4.15		3.21
6.	P1 x P7	3.98			27.15	11.38	20.93	4.45		5.82
7.	P2 x P3	-17.21			-8.28		0.30	-14.69		
8.	P2 x P4	-14.66			10.09		22.69	0.92		7.36
9.	P2 x P5	-10.69			-1.40		16.08	-9.27		1.57
10.	P2 x P6	-5.40			-10.93			-9.26		
11.	P2 x P7	-24.97			-8.75			-9.77		
12.	P3 x P4	-29.76			-4.41			-6.25		
13.	P3 x P5	17.06	7.49		24.84	15.34	27.01	28.95	17.26	17.01

14.	P3 x P6	18.55	6.09	-9.84			-2.26		
15.	P3 x P7	15.33	8.65	-13.53			20.47	19.66	
16.	P4 x P5	2.64		11.43	5.07	15.70	15.62	9.16	8.92
17.	P4 x P6	8.07		20.88	19.14	16.22	37.24	32.28	26.37
18.	P4 x P7	11.45	5.05	20.04	10.26	7.56	37.32	32.81	17.71
19.	P5 x P6	-23.50		-15.04			-11.81		
20.	P5 x P7	19.56	16.33	36.63	18.97	31.00	49.55*	36.83	36.53
21.	P6 x P7	4.49		24.82	16.19	10.08	26.03	17.64	12.39

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

4. CONCLUSION

Significant genetic diversity, which is essential for plant growth and yield traits, is demonstrated by the study on maize genotypes. This highlights the significance of both additive and non-additive genetic components in trait inheritance. The F1 hybrids P4x P3 and P3x P1, as well as the parental lines P1, P2, and P4, with their strong general combining ability (GCA), showed promise for improving yield qualities. Seven crossings (P1 x P6, P2 x P7, P2 x P5, P1 x P2, P3 x P4, P5 x P7, and P3 x P5) stand out in particular because their yields above those of the check hybrid, indicating their potential for increased output in future breeding programme. This study provides valuable insights for developing high-yielding maize hybrids, leveraging genetic diversity and strategic cross combinations.

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