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Combining ability and heterosis analyses for selected yield attributes in 7x7 diallel population of maize

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Abstract

An experiment was conducted with the objectives to study the combining ability and heterosis for plant height, cob height, kernel related traits hundred grain weight and test weight in maize during December to September 2020-2021. The experimental material was 7×7 diallel mating population (excluding reciprocal) consisted of seven parents and their 21 F₁'s. The results of simple analysis of variance (ANOVA) demonstrated that the parents and hybrids had enough genetic diversity. Moreover, analysis of variance for combining ability also exhibited significant general (GCA) and specific combining ability (SCA) for all the characters studied. The parent P5 was identified as the best general combiner for kernel related traits especially for test weight couple with hundred kernel weight. Regarding the hybrid combinations, hybrids P4 x P6 (281), P2 x P7 (165), P4 x P7 (155), P3 x P6 (142) and P2 x P5 (133) exhibited the best results for number of kernel per cob. The crosses P3 x P7 (6.62g), P1 x P7 (5.11g), P1 x P4 (5.07g), P1 x P2 (4.71g), and P3 x P6 (5.21g) performed best in terms of hundred grain weight while crosses P1 x P4 (4.84g), P2 x P6 (4.51g), P3 x P4 (4.33g), P1 x P2 (3.97g), and P1 x P3 (3.37g), were found to be extremely out yielded for the most important attribute, test weight. Considering the phenomena heterosis, the hybrids P4 x P6, P2 x P6, P2 x P4, P1 x P4, and P1 x P2 revealed significant heterosis over mid parent for kernel related parameters, and the crosses P3 x P7 (66.87g), P2 x P3 (63.89g), P1 x P3 (59.80g), P3 x P4 (55.32g). Nonetheless, P3 x P6 (55.16g) were the best cross combination for hundred kernel weight and in terms of test weight, P1 x P4 (50.23g), P2 x P4 (45.77g), P3 x P4 (47.23g) and P1 x P2 (44.03g) were the most desirable based on mid parent heterosis. Accordingly, for better parent heterosis the crosses P1 x P2 (41.25g, 44.03g), P1 x P3 (47.33g, 40.02g), P1 x P4 (49.70g, 50.23g), P3 x P7 (41.39g, 30.17g) and P3 x P4 (39.86g, 47.40g) expressed heterosis in desirable direction for hundred grain weight and test weight. Thus, parent P5 and the hybrids P3 x P4, P3 x P7, P1 x P3, P2 x P6, P3 x P6, P4 x P6, P1 x P2 may be selected as the best general and specific combiners respectively for maize variety development.

Keywords: Maize, hybrids, GCA, SCA, yield and heterosis

Introduction

Maize (*Zea mays L.*) is a highly adaptable crop that can thrive in diverse agro-climatic conditions. Maize is known as the "Queen of Cereals" worldwide due to its highest genetic yield potential among cereals. This plant is grown for human food, poultry and fish feed, biofuel, and industrial raw material. Roughly 4.5 billion people in 94 nations that are developing get at least 30% of their calories from maize, rice, and wheat. Hundreds of culinary and non-food products are made from every part of the plant, including grains, leaves, stalks, tassels, and even pith (shank). In 2016, it surpassed rice as Bangladesh's most significant cereal crop, pushing wheat to third place. The crop is presently grown on 4.47 lakh hectares of land, with an average yield of 8.7 tons per hectare, and 90% of the maize produced in the country is used to fuel a booming poultry and fish feed sector (The Daily Star, 2019). Globally, severe food insecurity has risen in recent years as a result of variety of factors, including human conflict, catastrophic climate occurrences, low export commodity prices reducing public investments, and food inequity. In 2017, around 770 million people, or nearly 10% of the world's population, were affected by extreme food insecurity. Maize demand is predicted to climb as the world's population grows and more people begin to consume more meat, poultry, and dairy products in their diets.

Maize will be the main crop in the developing world by 2025, According to the predictions, the demand for maize in developing countries is expected to increase twofold by the year 2050. Although Bangladesh's total food production has increased, the country still confronts substantial food security challenges due to the lack of diversification in food crop production. This causes individuals in the country to suffer from an unusually high rate of chronic and acute malnutrition, particularly among women and children. It is becoming increasingly clear that a true breakthrough in crop diversity is required to improve Bangladesh's economy. Hybrid maize could help to improve this situation, but because maize is a cross pollinated plant, it will require a series of field research. Maize plants that are inbred tend to have lower levels of vigor, which can result in a reduced potential for producing salable seeds. In addition, their ability to produce pollen may also be limited due to their weakened state. Although lines with good combining ability can be identified in the early stages of inbreeding, after several generations of self-fertilization, they may become too weak to be used effectively due to reduced grain yield or pollen production. Crossbreeding unrelated inbred lines produces genetically superior varieties that surpass their conventional parents. Hybrid maize provides higher yields, greater value, and lower production expenses. This is due to the hybrid vigor that occurs when two genetically unrelated inbred parents are crossed to create a hybrid. The result is stronger, bigger, and more robust plants. Additionally, brief few advantages of hybrid maize over inbred like, The objective is to rapidly identify distinct parental characteristics, achieve superior genotypes in a compressed period, leverage gene interactions in hybrid generation, and produce genetically uniform results. The goals are to reduce environmental interaction in F1 generation and to commercially produce hybrid maize seeds with positive impacts on the economy.

In the development of maize hybrids, parental line selection is critical. The diallel crossing approach can help breeders understand how genes are inherited in early filial generations. Which can help them generate hybrids (Hayman, 1954; Jinks, 1954) [19, 26]. Breeders can better understand gene action inheritance in early filial generations by using the diallel crossing approach (Hayman, 1954; Griffing, 1956) [19, 14]. In order to comprehend the genetic connections across various lineages, breeding programmes rely on genetic assessments of desirable features. To forecast the optimal pairings between parents and segregating populations, parallel crossings are frequently employed (Valério *et al.*, 2009; Baldissera *et al.*, 2012) [37, 2]. Sprague and Tatum (1942) [35], Hayman (1954) [19], and Griffing (1956) [14] introduced the idea of the diallel cross as a means of recombining the genetic variety present in the programme through crossings across all lineages. Additionally, diallel crosses enable the estimation of genetic factors, providing breeders with more knowledge and aiding in decision-making (Vencovsky, 1987) [38].

Plant breeding relies heavily on the understanding of the genetic relationships between crossings, which serves as the primary criterion for selecting combinations. To develop a progeny with a high genetic potential, selection based solely on desirable traits is inadequate. Finding genitors with a high combining capacity is essential for maximising the expression of heterosis in maize hybrids. To quantify the impacts of special combining ability (SCA) and general combining ability (GCA), one uses parallel analysis (Cruz Regazzi, 1994). With regard to genetic variants, GCA stands for additive x additive epistatic interaction and additive gene

action. Dominance and epistasis make up the majority of the non-additive variation categories that make up SCA (Griffing 1956b) [15]. Traits with greater additive genetic variance are probably more amenable to selection than are those with higher dominance genetic variance. Methodology for diallel cross analysis variance and effect estimates was presented by Griffing (1956a) [14]. Consequently, the goal of the current study was to estimate the heterosis with respect to better parents and mid parents as well as the combining skills (general and particular) of several maize inbreeds lines for yield components.

Materials and Methods

Experimental site and inbred Selection

The experiment was carried out in the research field and laboratory of Bangabandhu Sheikh Mujibur Rahman Agricultural University's Department of Genetics and Plant Breeding. We have (2016-2022) developed an "Inbred Pool" exploiting diverse exotic and local maize genotypes with superior characters. Subsequently, morphological as well as molecular dissection with SSR marker was also carried out to select the desire superior types. Thus, seven diverse inbreeds from the aforesaid inbred pool were exploited to generate diallel hybrid population. The parental genotypes utilized in this study were designated as P1, P2, P3, P4, P5, P6 and P7, which were chosen for their genetic diversity and diverse origins.

Development of single crosses and evaluation F₁ hybrid progeny

Experimental single cross hybrids were developed following 7 x 7 diallel cross fashion without reciprocal generating twenty one single cross combinations. Both parents and F1 hybrids were left in the field for attaining maturity. In the next growing seasons, the 21 F₁'s and 7 parental lines were grown in an RCB design with two replications spaced of 60 x 20 cm (between rows and hills) at the same location. In order to reduce the border impact, a single border row was employed at each replication end. Every row was 4 meters long. Observations were made on ten randomly chosen plants for growth parameters, yield contributing features, and quality parameters, and the entire suggested package of procedures was undertaken. The characters examined included plant height, cob height, no of kernel row per cob, no of row per cob, total kernel, kernel length, kernel breadth, kernel thickness, hundred grain weights and test weight.

Statistical analysis of the experimental data

According to the subjects and standard textbooks (Snedecor and Cochran, 1967; Clark, 1973) [33, 7], a preliminary statistical analysis of the data was conducted. Two primary methods were applied to the data in the diallel population (F₁) genetic analysis: Griffing's method and Hayman's method. Thus, an attempt was made to comprehend the genetic system governing significant qualities as well as general and specialised combining abilities. Several reference works (Mather and Jinks, 1987; Singh and Chaudhary, 1985; Dabholkar, 1982; Narain, 1993 and Falconer and Mackay, 1996) [26, 32, 9, 28, 11] provide their analytical techniques and processes, which are frequently mentioned with worked-out examples.

Combining ability analysis (Griffing's approach)

Griffing's (1956b) [15] methods 2, model 1 (fixed effect model) was used for combining ability analysis for each of the

trait. The experimental material in model 1 is considered the population from which inferences are to be drawn. The main goals are to compare the parents' combining skills and, by utilising the parents as testers, to determine which cross combination (s) is best.

Estimation of heterosis

The following equations were used to compare the mean of F₁ hybrids over mid parental value and higher parent in regard of a certain trait in order to determine the extent of heterosis (Rai, 1979).

$$\text{Percent of heterosis over mid parent (MP)} = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Percent of heterosis over higher parent (HP)} = \frac{\bar{F}_1 - \overline{HP}}{\overline{HP}} \times 100$$

Where,

\bar{F}_1 = Mean of any character of F₁ hybrids

\overline{MP} = The mid parental value, i.e. average of two parents

\overline{HP} = Mean of the higher parent

The test of significance for heterosis was done by usual statistical practice using the error variance from the ANOVA of F₁ and parental populations.

Results

Mean performance of the genotypes

The genotypes of every character showed significantly ($p < 0.01$) different genotypes. The parental genotype P2 (156cm) and the cross P2 x P7 (195cm) produced the tallest plants, while the parent genotype P1 (86cm) and the cross P1 x P4 (120cm) produced the shortest plants. However, medium to low plant height is desired for hybrid maize. Parent P2 (46cm) had the highest cob height, followed by P5 (42cm), while P4 (15cm) and P1 (23cm) had the lowest. Crosses P3 x P4 (65cm) and P2 x P7 (61cm) had the highest cob height, while P1 x P6 (27cm) and P1 x P4 (23cm) had the lowest (31cm). In respect of no of row/cob, the parental genotype P3 (14) followed by P7 (12) and cross P4 x P6 (17) displayed the highest row/cob and majority of the crosses produced good

significant row numbers. The parental genotypes P5 (18), P2 (15), and the cross P2 x P7 (36) had the maximum number of kernels per row, whereas the cross P2 x P5 (35) had a nearly same outcome. The crucial attribute total kernel/cob, parental genotypes P5 (198) and P3 (182), and the cross P4 x P6 (559) produced the maximum kernel/cob, and many crosses gave superior results. Kernel length was greatest in the P5 (9.90mm) paternal genotype and the P2 x P4 (12.42mm) hybrid. Kernel breadth was maximum in the parent genotype P5 (9.90mm) and the cross P2 x P4 (12.42mm). Kernel thickness was highest in the parent genotype P5 (9.84mm) and the cross P1 x P3 (5.87mm). Finally, the two essential yield-contributing traits, hundred grain yield and test weight, showed extremely close results in many crossings, which is beneficial for a breeder. In terms of hundred grain weight, the parental genotypes P5 (34.10gm) and P6 (25.23gm), as well as the cross P3 x P7 (34.81gm), followed by P1 x P2 (34.21gm), yielded the greatest results, while for test weight, the parent genotype P5 (38.82gm) and the cross P2 x P5 (39.95gm) are the best genotypes for future desirable hybrid maize production.

Analysis of variance

The analysis of variance (Table 3) showed that mean squares for the genotypes of single cross hybrid parents were significant at $p \leq 0.01$ for all the characters studied. The mean sum of squares of genotypes were highly significant for the characters-plant height (cm), cob height, number of row per cob, kernel per row, kernel per cob, hundred grains weight (g), test weight (g/100ml), kernel length (mm), kernel width (mm) and kernel thickness (mm). On the contrary, the analysis of variance (ANOVA) results for the quantitative traits of the genotypes that were tested are presented in (Table 4). All statistical analyses of studied morphological traits demonstrated considerable variance for all diallel cross features. Plant Height (cm), Cob Height (cm), No. of Rows per cob, No. of Kernel per row, No. of Kernel per cob, 100 seed weight (g), Test Weight (g/50ml), Kernel length (mm), Kernel breadth (mm), Kernel Thickness (mm), 100 seed weight (g), Test Weight (g/50ml), Kernel length (mm), Kernel breadth (mm), Kernel Thickness (mm) were highly significant (** $p < 0.01$).

Table 1: Mean values of different plant characters of the parents and hybrids of *Zea mays* diallel cross

Characters and Genotypes	Plant height (cm)	Cob height (cm)	No of rows/cob	No of kernels/row	Total kernel/cob	Kernel length (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Hundred kernel weight (g)	Test weight (g/50ml)
Parents										
P1	86	23	10	10.00	20.00	5.99	5.99	4.60	20.26	26.60
P2	156	46	8	15.00	40.00	8.05	8.05	3.99	24.22	27.68
P3	145	38	14	13.00	182.00	7.87	7.87	4.39	17.10	27.48
P4	129	15	8	8.00	32.00	8.84	8.84	4.16	21.35	26.20
P5	144	42	11	18.00	198.00	9.90	9.90	9.84	34.10	38.82
P6	146	34	6	9.00	12.00	6.76	6.76	7.70	25.23	28.76
P7	135	37	12	9.00	108.00	9.22	9.22	4.15	24.62	29.31
Hybrids										
P1xP2	149.67	34.33	13.33	21.67	289.00	10.33	10.33	5.79	34.21	39.09
P1xP3	144.50	42.50	11.25	23.25	262.25	8.92	8.92	5.87	29.85	37.86
P1xP4	120.67	31.33	12.67	21.33	268.00	10.90	10.90	4.77	31.96	39.66
P1xP5	146.25	39.50	15.50	22.75	354.75	10.66	10.66	5.03	29.25	38.82
P1xP6	132.00	27.50	6.50	8.50	55.50	8.01	8.01	4.65	25.02	33.48
P1xP7	168.20	45.00	11.80	21.40	260.20	10.31	10.31	5.07	32.69	37.05
P2xP3	168.00	49.00	14.00	26.00	361.20	10.55	10.55	5.11	33.86	36.95
P2xP4	167.80	49.80	14.00	27.00	375.60	12.42	12.42	4.73	32.62	39.27
P2xP5	188.40	55.00	13.40	34.60	462.00	11.27	11.27	4.67	32.62	39.95

P2xP6	171.60	42.20	14.40	24.60	354.80	11.95	11.95	4.49	29.40	39.61
P3xP4	170.50	65.00	14.00	29.00	400.50	11.54	11.54	4.13	29.86	39.56
P3xP5	163.00	38.33	11.00	32.33	357.67	10.15	10.15	5.07	33.59	39.71
P3xP6	157.40	45.20	14.20	30.60	435.20	11.54	11.54	4.63	32.84	36.89
P3xP7	178.20	58.80	12.40	34.40	425.40	11.25	11.25	4.63	34.81	36.96
P4xP5	138.80	39.00	12.80	25.80	326.80	10.39	10.39	4.52	26.22	39.18
P4xP6	187.33	56.67	17.00	32.67	559.00	12.05	12.05	5.46	28.57	37.64
P4xP7	174.07	51.53	14.70	32.73	483.10	11.33	11.33	5.00	27.14	38.07
P5xP6	179.20	45.80	11.40	29.80	333.80	9.83	9.83	4.73	29.32	37.85
P5xP7	177.00	51.00	10.50	32.00	334.00	9.66	9.66	4.72	25.36	39.61
P6xP7	177.60	40.60	12.60	21.80	277.20	9.84	9.84	5.10	24.58	36.02

Table 2: Analysis of variance (MS) for different plant characters in a 7 x 7 diallel cross of *Zea mays*

Source of variations	DF	Plant height (cm)	Cob height (cm)	No of rows/cob	No of kernels/row	Total kernel/cob	Kernel length (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Hundred kernel weight (g)	Test weight (g/50ml)
Replication	1	1147.35	184.76	47.17	2017.59	4831.50	53.24	15.13	8.28	171.25	274.93
Genotype	27	1150.60**	258.22**	13.98**	159.08**	48063.70**	5.06**	1.51**	2.77**	43.82**	42.97**
Error	27	12.56	1.88	0.37	0.0006	411.50	0.04	0.02	0.02	0.15	0.01

** $p < 0.01$ **Table 3:** Analysis of variance (MS) for combining ability for different plant characters in a 7 x 7 diallel cross of *Zea mays*

Item	DF	Plant height (cm)	Cob height (cm)	No of rows/cob	No of kernels/row	Total kernel/cob	Kernel length (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Hundred kernel weight (g)	Test weight (g/50ml)
GCa	6	1295.46**	200.98**	3.90**	72.00**	16676.02**	2.72**	1.22**	2.16**	11.97**	15.06**
SCa	21	369.54**	108.57**	7.87**	81.69**	26133.52**	2.47**	.62**	1.16**	24.76**	23.32**
Error	27	6.28	0.94	0.18	0.0003	205.75	0.02	0.01	0.01	0.07	0.01
gca:sca	0.28	3.50	1.85	0.49	0.88	0.63	1.10	1.96	1.86	0.48	0.64

** $p < 0.01$

Combining ability effects (Griffing's approach)

Using Griffing's Method II Model I, genetic analysis was conducted. GCA and SCA variance were found to be extremely significant for the majority of the characters examined in the F1 generation, according to combining ability analysis.

General combining ability (GCA) effects

The General Combining Ability (GCA) effects of parental single cross hybrid lines for ten characters are shown in Table 5. There was a great deal of variation in the GCA effects between the parents. In this study, parental lines with substantial and negative GCA impacts were deemed to be good general combiners based on their plant height and cob height. The usage of these parents and significant and negative GCA plant and cob heights may be helpful in the development of early and small stature hybrid variety(s). Conversely, those with significant and positive GCA impacts were thought to be strong general combiners for yield and other yield components (Begum *et al.*, 2018) [4]. For the present study, yield and yield contributing main traits are number of kernel per cob, test weight, 100seeds weight,

kernel length, kernel width, kernel thickness etc. P1 showed significant and negative GCA effect for the traits plant height (-24.98) and cob height (-8.63) indicating its potentiality for developing early and short stature hybrid variety(s). For most of the yield and yield contributing traits parental line P5 showed significant and highest positive effects of GCA. P5 was identified as a good combiner for exhibiting significant and highest GCA effects for number of kernel per cob (29.37), number of kernel per row (3.07), kernel length (0.18), kernel breadth (0.42), and kernel thickness (0.89). For trait number of kernel per cob P5 exhibited highest positive and significant GCA effects (29.37) followed by P2 (11.81). In case of test weight/50ml P5 (2.80) and P2 (0.11) exhibited highest GCA effect which is considered as one of the most important criterion for hybrid development. P5 and P2 were good combiners for 100grains weight with a GCA effect 1.71 and 1.49 respectively. P5 is a good combiner for kernel breadth trait with highest (0.42) GCA effects followed by P7 (0.35) and P5 was also marked as good for kernel thickness properties having highest (0.89) effects of GCA followed by P6 (0.45). So considering all yield contributing traits P5 parental line shows better result than any other parental line.

Table 4: Estimates of general combining ability (GCA) effects for different plant characters in a 7 x 7 diallel cross of maize

Characters and Parents	Plant Height (cm)	Cob Height (cm)	No of rows/cob	No of kernels/row	Total kernel/cob	Kernel length (mm)	Kernel breadth (mm)	Kernel thickness (mm)	Hundred kernel weight (g)	Test weight (g/50ml)
P1	-24.75 **	-8.63 **	-0.70 **	-5.20 **	-85.66 **	-1.00 **	0.21 **	-0.01 ns	-0.63 **	-0.93 **
P2	10.70 **	4.43 **	0.24 ns	1.53 **	11.81 *	0.37 **	-0.06 ns	-0.35 **	1.49 **	0.11 **
P3	1.73 *	3.44 **	0.83 **	1.77 **	33.95 **	-0.05 ns	0.06 ns	-0.25 **	-0.02 ns	-0.52 **
P4	-4.31 **	-2.28 **	0.42 **	-0.13 **	19.59 **	0.69 **	-0.50 **	-0.39 **	-1.12 **	-0.19 **
P5	2.74 **	0.75 *	-0.09 ns	3.07 **	29.37 **	0.18 **	0.42 **	0.89 **	1.71 **	2.80 **
P6	4.57 **	-1.99 **	-1.03 **	-2.19 **	-29.02 **	-0.37 **	-0.47 **	0.45 **	-1.00 **	-0.95 **
P7	9.32 **	4.28 **	0.33 *	1.14 **	19.96 **	0.17 **	0.35 **	-0.34 **	-0.44 **	-0.32 **

Table 5: Estimates of specific combining ability (SCA) effects for different plant characters in a 7 × 7 diallel cross of *Zea mays*

Characters Crosses	Plant height (cm)	Cob height (cm)	No of rows/cob	No of kernels/row	Total kernel/cob	Kernel length (mm)	Kernel breath (mm)	Kernel thickness (mm)	Hundred kernel weight (g)	Test weight (g/50ml)
P1xP2	6.72 **	-4.45 **	1.62 **	2.12 **	75.27 **	0.94 **	0.42 **	1.09 **	4.71 **	3.97 **
P1xP3	10.51 **	4.71 **	-1.05 **	3.47 **	26.38 **	-0.05 ns	-0.71 **	1.07 **	1.85 **	3.37 **
P1xP4	-7.27 **	-0.74 ns	0.78 **	3.45 **	46.49 **	1.20 **	-0.02 ns	0.11 **	5.07 **	4.84 **
P1xP5	11.26 **	4.40 **	4.12 **	1.67 **	123.46 **	1.46 **	-0.53 **	-0.90 **	-0.48 **	1.01 **
P1xP6	-4.82 **	-4.86 **	-3.94 **	-7.32 **	-117.40 **	-0.63 **	0.01 ns	-0.85 **	-2.00 **	-0.59 **
P1xP7	26.63 **	6.38 **	-0.00 ns	2.25 **	38.32 **	1.12 **	0.76 **	0.36 **	5.11 **	2.36 **
P2xP3	-1.43 ns	-1.85 **	0.76 **	-0.51 **	27.85 **	0.21 **	0.73 **	0.65 **	3.74 **	1.42 **
P2xP4	4.42 **	4.67 **	1.17 **	2.38 **	56.61 **	1.34 **	0.06 ns	0.41 **	3.61 **	3.41 **
P2xP5	17.96 **	6.83 **	1.08 **	6.79 **	133.23 **	0.70 **	-0.10 *	-0.92 **	0.78 **	1.10 **
P2xP6	-0.67 ns	-3.23 **	3.02 **	2.05 **	84.42 **	1.94 **	0.31 **	-0.66 **	0.26 *	4.51 **
P2xP7	17.78 **	9.71 **	1.65 **	9.72 **	165.04 **	0.29 **	0.28 **	0.18 **	1.70 **	2.55 **
P3xP4	16.08 **	20.86 **	0.58 **	4.15 **	59.37 **	0.88 **	0.93 **	-0.29 **	2.35 **	4.33 **
P3xP5	1.53 ns	-8.84 **	-1.92 **	4.29 **	6.76 ns	-0.00 ns	0.25 **	-0.62 **	3.25 **	1.48 **
P3xP6	-5.90 **	0.76 ns	2.23 **	7.81 **	142.69 **	1.95 **	0.71 **	-0.63 **	5.21 **	2.41 **
P3xP7	10.15 **	8.10 **	-0.94 **	8.28 **	83.91 **	1.11 **	1.33 **	0.16 **	6.62 **	1.86 **
P4xP5	-16.62 **	-2.45 **	0.29 ns	-0.35 **	-9.75 ns	-0.50 **	-0.38 **	-1.03 **	-3.02 **	0.63 **
P4xP6	30.08 **	17.95 **	5.44 **	11.77 **	280.84 **	1.72 **	0.63 **	0.35 **	2.04 **	2.84 **
P4xP7	12.06 **	6.56 **	1.77 **	8.51 **	155.97 **	0.45 **	0.34 **	0.68 **	0.05 ns	2.65 **
P5xP6	14.89 **	4.05 **	0.35 ns	5.71 **	45.86 **	0.01 ns	0.85 **	-1.66 **	-0.04 ns	0.05 ns
P5xP7	7.94 **	2.99 **	-1.92 **	4.58 **	-2.91 ns	-0.71 **	-0.54 **	-0.88 **	-4.56 **	1.19 **
P6xP7	6.71 **	-4.67 **	1.12 **	-0.36 **	-1.32 ns	0.03 ns	-0.55 **	-0.06 ns	-2.63 **	1.35 **

Specific combining ability (SCA) effects

The selection of parental material for hybridization might be aided by SCA effects when high yielding specific combinations are needed, particularly in the production of hybrid maize. Major SCA effects were found for grain ear, grain yield, and biological features, indicating partial dominance and dominance types of gene activity. As a result, choosing certain cross combinations is more crucial. In addition, early generation selection for these traits will be more successful, and hybrid development can profit from this (Zakiullah *et al.*, 2019) [39]. According to the favourable SCA impacts, breeders would find those particular combinations helpful in improving the characteristics they are looking for in a maize breeding programme. Favourable combinations of dominance effects when those parents are crossed result in hybrids with strong positive SCA. Because negative values indicate a reduction in leaf angle compared to the parents, negative SCA pairings would also be helpful for improving leaf angle for intercropping compatibility. Positive SCA show that a characteristic has increased in comparison to the parents for that particular trait (Jatasra *et al.* 1980; Kang *et al.* 1995) [22, 25]. The distinct combining ability impacts indicate how non-additive gene activity contributes to the characters' expression. Although high SCA can also result from low x low, low x medium, or high x medium combinations, it indicates the extremely precise combining capacity that leads to the maximum performance of select specific cross combinations. Generally speaking, a substantial portion of the SCA effects observed in low x low crosses may be attributed to non-allelic gene activity that produces over-dominance when a dominance x dominance type is present and cannot be fixed. Epistatic interaction appears to have a major role in the improved performance of most hybrids (Begum *et al.*, 2018) [4].

Plant height (cm)

Negative SCA effect is desirable for hybrid development since it allows for decreased plant height. Table 6 showed that 14 crosses among the 21 crosses exhibited significant positive SCA effects for the trait plant height. The highest negative

SCA effect were estimated from the cross P4 x P5 (-16.62) indicating that this combination might be suitable for evolving genotypes possessing shorter plant height. As results demonstrated, few other cross combinations, such as P1 x P4, P3 x P6, and P1 x P6, also presented opportunities for developing stature plants.

Cob height (cm)

Table 6 shows that 12 of the 21 cross combinations for the trait cob height had substantial positive SCA effects. The cross combination, P3 x P4 (20.86) showed the highest and positive SCA effects followed by P4 x P6 (17.95). The highest negative SCA effect were estimated from the cross P3 x P5 (-8.84) followed by P1 x P6 (-4.86) for evolving shorter cob height. Positive association between ear height and grain height was reported by Halidu *et al.*, (2015) [18] indicating that increase in ear height contributed to increase grain yield. Only P3 x P6 and P1 x P4 are non-significant, whereas all other crosses are significant at the 1% level.

Number of kernel rows per cob

Table 6 shows that for the number of kernel rows per cob, 12 of the 21 crosses had significant positive SCA impacts. For this characteristic, a positive sca value is required; when the row number increases, the yield will automatically increase. P4 x P6 (5.44) had the highest and most beneficial SCA effects, followed by P1 x P5 (4.12) and P2 x P6 (5.42). The cross P1 x P6 (-3.94) had the greatest negative SCA effect due to the ensuing lesser number of rows per cob, followed by P3 x P5 (-1.92) and P5 x P7 (-1.92). SCA effects were found to be non-significant in maize cross combinations P4 x P5 (0.29ns), P1 x P7 (-0.00ns), and P5 x P6 (0.35ns).

Kernel Number per row

Four crosses among the 21 crosses exhibited significant negative SCA effects for the trait kernel per row (Table 6) and positive cross combination, P4 x P6 (11.77) demonstrated the highest positive and significant SCA effects followed by P2 x P7 (9.72) and P3 x P7 (8.28). The highest negative SCA effect were estimated from the cross P1 x P6 (-7.32) for resulting

lesser number of kernel per row followed by P2 x P3 (-0.51), P6 x P7 (-0.36) respectively. The number of grains or kernels per row and the weight of 100 grains have a large direct impact on grain output in both genetic groups, according to Teodoro *et al.* (2014) [36]. Thus why P4 x P6 can be considered as a good combiner for this trait and at the 1% level of significance, all of the hybrid crossings sca were significant.

Kernel number per cob

Among the 21 crosses, eight crosses expressed significant positive SCA effects for the trait kernel per cob. The cross combination, P4 x P6 (280.84) showed the highest positive significant SCA effects followed by P2 x P7 (165.04) and P4 x P7 (155.97). As KPC is one of the most important components rendering yield, these cross combinations with positive SCA signifying their candidacy for the development of genotype with higher yield.

Kernel length

Significant positive SCA effects for kernel length was recorded in P3 x P6 (1.95) followed by P2 x P6 (1.94) and P4 x P6 (1.72) resulted in producing bigger kernel. The cross combination, P5 x P7 (-0.71) showed the highest and negative SCA effects followed by P1 x P6 (-0.63) and P4 x P5 (-0.50) respectively. P1 x P3 (-0.05), P5 x P6 (-0.03), P6 x P7 (-0.01) and P3 x P5 (-0.00) produced non-significant SCA effects.

Kernel breadth

Significant positive SCA effects for kernel length was recorded in P3 x P7 (1.33) followed by P3 x P4 (0.93) and P5 x P6 (0.85) resulted in producing wider kernels. The cross combination, P1 x P3 (-0.71) showed the highest and negative SCA effects followed by P6 x P7 (-0.55) and P5 x P7 (-0.54) and P3 x P5 (-0.53) respectively. Again P1 x P4 (-0.02), P1 x P6 (0.01), P2 x P4 (0.06) produced non-significant SCA effects.

Kernel thickness

Significant positive SCA effects for kernel length was recorded in P1 x P2 (1.09) followed by P1 x P3 (1.07) and P4 x P7 (0.68) resulted in producing thicker kernels. The cross combination, P5 x P6 (-1.66) showed the highest and negative SCA effects followed by P4 x P5 (-1.03) and P2 x P5 (-0.92) respectively. However, only one cross P6 x P7 (-0.06) produced non-significant SCA effects.

Hundred kernel weight (gm)

One of the most essential grain characteristics is the hundred grain weight. A plant's ultimate grain output is mostly determined by 100 grain weight, as well as a variety of other component features (Netravati *et al.*, 2013) [29]. Teodoro *et al.* (2014) [36] found a high direct effect of 100 grain weight on total grain weight, and Sesay *et al.* (2017) [31] found a positive and significant association of 100 grain weight with grain yield at both the genotypic and phenotypic levels, indicating that these traits are important yield components. 14 crosses among the 21 crosses exhibited significant positive SCA effects for the trait hundred kernel weight (Table 6). The cross combination, P3 x P7 (6.62) revealed the highest and positive SCA effects followed by P3 x P6 (5.21) and P1 x P7 (5.11) signifying that these could be considered as good combiners contributing to increase total grain yield of maize.

Test weight (gm/50ml)

It will be most desired if any cross combination has the greatest positive test weight as well as the highest 100 grain weight. Except for one cross (name the cc), the all of the cross combinations had a significant and positive SCA effect for test weight. P1 x P4 (4.84) had the highest and positive SCA effects, followed by P2 x P6 (4.51) and P3 x P4 (4.33). At a 1% level of significance, the only negative SCA effect was assessed from the cross P1 x P6 (-0.59) for evolving lowest test weight.

Magnitude of Heterosis

In Table 7, the heterosis was calculated for each of the seventeen characters that were crossed across the mid-parent (MP) and better parent (BP). Recessiveness ranged from partial to under-recessive, whereas dominance ranged from partial to over-dominance when the values of the ratio were negative (Solieman *et al.*, 2013 & Begum *et al.*, 2017) [34, 3].

Plant height

The extent of significantly heterosis over mid-parent (MP) ranged from 8.18% to 52.22% while only one cross was found non significant for mid parents heterosis. Significant heterosis in negative direction over MP was not found in this trait. Heterosis over better parent (BP) ranged from -6.46% to 28.94% depending on the crosses and apparently all of the crosses except P1 x P4 and P1 x P6 showed negative heterosis over better parent (BP). The highest negative heterosis for plant height was recorded in the cross P1 x P4 followed by the crosses P1 x P6. Therefore "P1 x P4" cross could be considered as the most promising for this trait.

Table 6: Percentage of heterosis over mid and better parent for different yield attributes in 7x 7 diallel population of maize

Hybrids	Plant height (cm)		Cob Beet (cm)		Kernel Row/Cob		No of Kernel/Row		No of Kernel/Cob		Kernel Length (cm)	
	HOMP (%)	HOMP (%)	HOMP (%)	HOBP (%)	HOBP (%)	HOBP (%)	ROMP (%)	HOBP (%)	HOMP (%)	HOBP (%)	HONIP (%)	HOBP (%)
P1xP2	23.69**	-4.06 ns	-0.49 ns	-25.37**	48.13**	33.32**	73.35**	44.46**	863.33	622.50	47.12**	28.29**
P1xP3	25.11**	-0.34 ns	39.34**	11.84**	-6.25 ns	-19.64**	102.17**	78.85**	159.65	44.09**	28.72**	13.34**
P1xP4	12.25**	-6.46 *	64.90**	36.22**	40.76**	26.68**	137.02**	113.32**	930.77	737.50**	47.00**	23.30**
P1xP5	27.17**	1.56 ns	23.44**	-3.66 ns	47.62**	40.91**	62.50**	26.39**	225.46**	79.17**	34.14**	7.65**
P1xP6	13.79**	-9.59**	-3.51 ns	-19.12**	-18.75**	-35.00**	-10.53**	-15.00**	246.88	177.50 ns	25.65**	18.49**
P1xP7	52.22**	24.59**	50.00**	21.62**	7.27 ns	-1.67 ns	125.26**	114.00**	306.56	140.93**	35.54**	11.80**
P2xP3	11.63**	7.69**	16.67**	6.52*	27.27**	0.00 ns	85.71**	73.33**	225.41**	98.46**	32.54	31.06**
P2xP4	17.75**	7.56**	63.28**	8.26 *	75.00**	75.00**	134.78**	80.00**	943.33**	839.00**	47.04**	40.47**
P2xP5	25.60**	20.77**	26.44**	19.57**	41.05**	21.82**	109.70**	92.22**	288.24	133.33**	25.57**	13.84**
P2xP6	13.64**	10.00**	5.50 ns	-8.26 *	105.71**	80.00**	105.00**	64.00**	1264.62**	787.00**	61.34**	48.42**
P2xP7	33.88**	24.87**	47.95**	33.48**	44.00**	20.00**	196.67**	137.33**	554.59	348.52**	25.62**	17.65**
P3xP4	24.45**	17.59**	145.28**	71.05**	27.27**	0.00 ns	176.19**	123.08**	274.30**	120.05**	38.12**	30.54**
P3xP5	12.80**	12.41**	-2.96 ns	-6.51 ns	-12.00**	-21.43**	108.59**	79.62**	88.25**	80.64**	14.21**	2.50 ns

P3xP6	8.18 **	7.81 **	25.56 **	18.95 **	42.00**	1.43 ns	178.18 **	135.38 **	348.66	139.12 **	57.72 **	46.60 **
P3xP7	27.29 **	22.90 **	56.80 **	54.74 **	-4.62 ns	-11.43'	212.73 **	164.62 **	193.38	133.74 **	31.63 **	21.99 **
P4xP5	1.68 ns	-3.61 ns	39.29 **	-4.88 ns	34.74 **	16.36 **	98.46 **	43.33 **	184.17 **	65.05 **	10.86 **	4.92 •
P4xP6	36.24**	28.31 **	131.30 **	66.67 **	142.86 **	112.50 **	284.33 **	262.98 **	2440.91	1646.88	54.49 **	36.31 **
P4xP7	31.87 **	28.94 **	98.21 ••	39.28 **	47.00 **	22.50**	285.10 **	263.70 **	590.14	347.31 **	25.42 **	22.83 **
PSxP6	23.59 **	22.74**	22.13 **	11.71 **	34.12 **	3.64 ns	120.74 **	65.56 **	217.90 **	68.59 **	18.01 **	-0.71 ns
PSxP7	26.88**	22.92**	30.77**	24.39**	-8.70 n\$	-12.50 •	137.04**	77.78**	118.30**	68.69**	1.02 ns	-2.45 ns
P6xP7	26.41 ••	21.64**	14.37 **	9.73 •	40.00 **	5.00 ns	142.22 **	142.22 **	362.00 **	156.67 **	23.15 **	6.72 **

HOMP: Heterosis over Mid parent; HOBP: Heterosis over Better parent; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

Table 6: (Contd.)

Hybrids	Kernel breadth (cm)		Kernel thickness (cm)		Hundred kernel weight (g)		Test weight (g/50m1)	
	ROMP (%)	HOBP (%)	ROMP (%)	HOBP (%)	ROMP (%)	ROMP (%)	ROMP (%)	ROMP (%)
P1xP2	9.11"	1.30 ns	34.75"	25.82••	53.82••	41.25••	44.03••	44.03••
P1xP3	0.93 ns	-9.07 "	30.59 "	27.61 "	59.80 "	47.33 "	40.02 "	40.02 "
P1xP4	4.10••	-7.65**	8.90••	3.70 ns	53.62••	49.70••	50.23"	50.23••
P1xP5	-6.53••	-9.30••	-30.33••	-48.88••	7.62••	-14.22••	18.68••	18.68••
P1xP6	5.66**	-7.11"	-24.43"	-39.64••	9.99"	-0.84 ns	20.94 "	20.94**
P1xP7	12.06••	8.82••	15.83••	10.16••	45.68••	32.78••	32.53••	32.53••
P2xP3	24.02"	20.05"	21.90••	16.34••	63.89 "	39.80••	33.98"	33.98"
P2xP4	10.90**	5.58••	16.07••	13.70••	43.16••	34.68••	45.77••	45.77••
P2xP5	2.17 ns	-7.74 "	-32.47 "	-52.54 "	11.87 "	-4.34 "	20.15 "	20.15"
P2xP6	15.39 "	8.75 "	-23.18 "	-41.69 "	18.91 "	16.53 "	40.36 "	40.36 "
P2xP7	12.51**	7.42**	11.55••	9.40••	28.54••	27.50••	34.30••	34.30••
P3xP4	27.40 "	25.22 "	-3.45 ns	-5.98 •	55.32 "	39.86 "	47.40 ••	47.40 ••
P3xP5	10.27 "	-3.27 •	-28.74 "	-48.48 "	31.21 "	-1.50 ns	19.79 "	19.79 "
P3xP6	26.12 "	22.69 "	-23.45 "	-39.90 "	55.16 "	30.16 "	31.19 "	31.19 "
P3xP7	29.69"	20.04••	8.37••	5.41 ns	66.87••	41.39••	30.17••	30.17••
P4xP5	-1.13 ns	-14.56 "	-35.46 "	-54.09 "	-5.43 "	-23.11 "	20.52 "	20.52 "
P4xP6	20.13 "	18.86 "	-7.97 "	-29.12 "	22.67 "	13.24 "	36.97 "	36.97 "
P4xP7	13.47 "	3.37 •	20.28 "	20.13 "	18.06 "	10.22 "	37.18 "	37.18 "
P5xP6	13.73"	-2.58 ns	-46.09••	-51.96"	-1.16 ns	-14.02"	12.02**	12.02**
P5x177	-2.48 In	-8.03 "	-3232 "	-52.03 "	-13.62 "	-25.63 "	16.28 "	16.28 "
P6xP7	4.21 "	-5.96 "	-13.92 "	-33.77 "	-1.38 ns	-2.58 ns	24.06 "	24.06 "

HOMP: Heterosis over Mid parent; HOBP: Heterosis over Better parent; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

Cob height

Negative heterosis is desirable for the height related traits. The heterosis over BP ranged from -8.26% for P2xP4 to 71.05% for P3 x P4. Three crosses viz. P1 x P2, P1 x P6 and P3 x P5 out of 21 crosses exhibited non-significant negative heterosis over MP. On the contrary, three crosses out of 21 crosses showed negative heterosis over BP and only two (P3 x P5, P4 x P5) of which gave non-significant value.

No of kernel row per co Heterosis over MP ranged from 27.27% to 142.86% but over BP it ranged from 11.43% to 112.50%. In case of heterosis over MP 15 crosses out of 21 crosses exhibited positive heterosis, whereas over better parent ten crosses showed significant positive heterosis for kernel row and the highest positive heterosis over BP and MP was 112.50% and 142.86% in P4 x P6 cross.

No of kernel per row

Positive heterosis is desirable for kernel related traits. Positive heterosis over mid-parent was observed for 20 hybrids out of 21 and among them the crosses P4 x P6, P4 x P7 and P3 x P7 were appeared to be the most desirable due to their highest positive heterotic effect. Heterosis over better parent (BP) ranged from -15.00% to 263.70% and almost all crosses (20 out of 21 crosses) exhibited positive heterosis over BP. Thus, the expression of heterosis for kernel per row was far wide. The highest positive heterosis (263.70%) over BP was recorded in the cross P4 x P7, whereas the crosses P4 x P6 and P3 x P7 also exhibited good results (around 90%).

No of kernel per cob

The lowest and highest heterosis over mid parental value for

individual crosses were 88.25% for P3 x P5 to 2440.91% for P4 x P6. No negative heterosis were observed for heterosis over mid parents (MP) The range of heterosis over BP was -44.09% to 1646.84%, the lowest and highest estimates were in P1 x P3 and P4 x P6, respectively. All of the hybrids showed positive significant results but seven (viz. P4 x P6, P2 x P4, P2 x P6, P1 x P4, P1 x P2, P2 x P7 and P4 x P7) showed highest positive heterosis over better parents. Only the P1xP6 cross showed non-significant heterosis over better parental value.

Kernel length

All the crosses showed positive heterosis over mid parent except one cross (P5 x P7) which was highly significant ($p < 0.01$). The positive heterotic effects over mid-parent ranged from 10.86% for P4 x P5 to 61.34% for P2 x P6, while one cross P5 x P7 (1.02) out of 21 crosses showed non-significant heterosis over mid-parent. Heterosis over BP ranged from 4.92% to 48.42% and two crosses out of 21 showed negative non-significant heterosis and one cross (P3 x P5) showed non-significant positive heterosis. Six crosses viz. P2 x P6, P3 x P6, P2 x P4, P4 x P6, P2 x P3 and P3 x P4 showed highly significant ($p < 0.01$) positive heterosis over BP. One cross (P4 x P5) showed positive heterosis at 5% level of significans. The highest percentage of heterosis was recorded for P2 x P6 followed by P3 x P6.

Kernel breadth

The estimates of heterosis for individual crosses (Table 7) revealed that all of the hybrids except one cross (P1 x P6) showed negative significant and four crosses (P1 x P3, P2 x

P5, P4 x P5 and P5 x P7) showed non-significant ($P < 0.01$) heterosis over mid-parent. The highest (29.69%) and lowest (4.10%) positive heterosis over mid parent was obtained for P3 x P7 and P1 x P4, respectively. Over BP heterosis ranged from -3.27% for P3 x P5 to 25.22% for P3 x P4. In case of heterosis over BP nine crosses out of 21 showed negative heterosis (Table 7). In the case of BP heterosis, only two crosses are non-significant, one (P1 x P2) is positive non-significant and the other (P5 x P6) is negative non-significant.

Kernel thickness

Positive heterosis is preferable for these traits, however at a 5% level of significance; negative heterosis is detected in more crossings (11) than positive heterosis. The extent of heterosis over MP varied from -46.09% to 34.75%. Over MP, eleven of the 21 crosses had highly significant negative heterosis, nine had positive significant heterosis. The estimated maximum heterosis over mid parent was obtained in the cross P1 x P2 followed by P1 x P3. Heterosis over BP ranged from -54.09% to 27.61% and over better parent, the cross P1 x P3 (27.61) demonstrated the most positive heterosis, followed by P1 x P2 (25.82) and P4 x P7 (20.13). Only 7 of the 21 crosses demonstrated positive heterosis over the better parent, with two being non-significant and 12 being negative heterosis.

Hundred grain weight

Although the hundred grain weight and test weight are important factors in determining a maximum yield measurement, which is usually desirable for a breeder, almost all crosses showed significant ($P < 0.05-0.01$) positive heterosis, with the exception of two crosses (P4 x P5, P5 x P7) that were negatively significant. The lowest and highest heterosis over mid parent (MP) was recorded P3 x P7 (66.87%) followed by P1 x P3 (59.80%), P1 x P2 (53.82%), P1 x P4 (53.62%), P3 x P4 (55.32%) and P3 x P6 (55.16%). The extent of heterosis over better parent (BP) ranged from -25.63% to 49.70%. Significant positive heterosis was showed by 13 crosses out of 21 crosses. The cross P1 x P4 (49.70%) showed the highest positive heterosis over better parent which was followed by P1 x P3 (47.33%), P1 x P2 (41.25%), P3 x P7 (41.39%) and P3 x P4 (39.86%).

Test weight

A cross will be a preferable alternative for hybrid maize production in the future due to its high significant test weight. Heterosis over mid-parent ranged from 12.02% for P3 x P6 to 50.23% for P1 x P4. The crosses P3 x P4 (47.40%), P2 x P4 (45.77%) and P1 x P2 (44.03%) also gave good result. However no negative heterosis was found over MP and better parent. Over better parent heterosis ranged from 12.02% to 50.23% just like mid parent. The highest positive heterosis were recorded for the crosses P1 x P4 (50.23%) followed by P3 x P4, P1 x P4 and P1 x P2. Therefore cross P1 x P4 as well as P3 x P4, P2 x P4 and P1 x P2 could be considered as the most promising for this trait.

Discussion

The presence of genetic diversity and divergence across individuals was indicated by the considerable variance seen in the trait values (Chauhan *et al.*, 2019) [6]. Additionally, Ferdoush *et al.* (2017) [12] discovered a significantly significant variance in the following measurements: plant height (cm), cob height (cm), cob length (cm), cob width (cm), number of kernels per cob, and 1000-kernel weight (g).

In 2019, Sultana also determined highly significant differences for these traits in maize inbred lines. Similar results were also determined by Chandel & Guleria (2019) [5]. In a different research, said that there is substantial variance in the number of rows per cob, the number of kernels per row, and the weight of 100 kernels.

The combination ability studies conducted using Griffing's methodology demonstrated substantial variations in gca and sca ($P < 0.01$) for every character examined, suggesting that both additive and non-additive gene activities contribute to the inheritance of these traits. In terms of kernel row per cob, kernel number per cob, hundred grain weight, and test weight, the non-additive genetic component was exclusive or predominate. Following a combining ability examination, parents were classified as (i) average combiners for intermediate gca effects between highest and lowest values; (ii) bad combiners for lowest values of gca effects; and (iii) strong combiners for highest gca effects. The importance of additive gene activity was proven by the GCA: SCA ratio. Because additive genetic variation predominates in this feature, the parent could be chosen based on GCA values. The trait's predominance of additive genetic variance also means that, in addition to hybrid and synthetic breeding, there is the possibility of genetic improvement by selection of favorable alleles. Specific combiners (crosses) were also established into identical groups for distinct plant traits based on sca impacts. For all of the characters studied, the gca and sca variances were extremely significant ($P < 0.01$) in the evaluation of variances for combining ability (Table 4). Furthermore, all of the characters had a gca:sca ratio greater than one, indicating that they were primarily under additive genetic control. Accordingly, line attributes and line behaviour in a particular hybrid combination are regarded as crucial for assessing an inbred line in the development of hybrid maize.

The heterosis over mid parent and better parent were estimated for plant height, cob height and other kernel related characters, hundred grain weight and test weight in maize. Cross combinations and the traits being studied were discovered to influence the kind and degree of heterosis in both types (over mid-parent and better parent). For several hybrid characteristics, both positive and negative midparent heterosis was found; nevertheless, only a small number of hybrids had noteworthy and desired values. The cross P1 x P7 (53cm) had the highest positive mid parent heterosis for plant height, and P3 x P4 (145cm) had the highest positive mid parent heterosis for cob height. In terms of plant and cob height, there was no evidence of negative significant mid parent heterosis. Three characteristics, namely the number of kernel rows per cob, kernels per row, and total kernel, revealed the most significant positive heterosis. For many hybrid traits, both positive and negative better parent heterosis was achieved, with only a few hybrids showing significant and desirable values. In hybrid, P1 x P6, negative heterosis over better parent was detected in both plant height (-9.69cm) and cob height (-19.12cm). Aside from this, other traits associated with yield-contributing qualities significant positive value are particularly desirable for hybrid maize. Finally, hybrids P1 x P4, P1 x P2, P1 x P3, P1 x P6, P3 x P7, and P4 x P6 can be chosen for commercial use of maize. The F₁ population of Ji *et al.* (2006) [24], Devi *et al.* (2007) [10], and Frascaroli *et al.* (2007) [13] all reported varying ratios of heterotic values for plant height.

Because of delayed pollination and little to no grain filling, plants with the cob positioned high yield less grain (Munib *et*

al., 2013)^[27].

Conclusion

The GCA greater than the SCA in all characters except kernel row per cob, kernel per row, total kernel, hundred grain weight and test weight which revealed the importance of both additive and non-additive gene action. The parent P5 was found to be the best desirable general combiner, whereas the hybrids P4 x P6 (281), P2 x P7 (165), P4 x P7 (155), P3 x P6 (142) and P2 x P5 (133) exhibited the best particular selections for total kernel per cob. The crosses P3 x P7 (6.62g), P1 x P7 (5.11g), P1 x P4 (5.07g), P1 x P2 (4.71g), and P3 x P6 (5.21g) performed best in terms of hundred grain weight. Among these crosses P1 x P4 (4.84g), P2 x P6 (4.51g), P3 x P4 (4.33g), P1 x P2 (3.97g), and P1 x P3 (3.37g), was found to be extremely significant for the most important farmers preferred attribute, test weight. For hundred grain weight and test weight, the crosses P1 x P2 (41.25g, 44.03g), P1 x P3 (47.33g, 40.02g), P1 x P4 (49.70g, 50.23g), P3 x P7 (41.39g, 30.17g), and P3 x P4 (39.86g, 47.40g) demonstrated significant heterosis over the better parent.

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