Annals of Bangladesh Agriculture
Journal homepage: bsmrau.edu.bd/aba

ORIGINAL ARTICLE

Genetic analysis of selected quantitative attributes in maize genotypes exploiting 6 × 6 diallel mapping population

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ARTICLE INFO.

Keywords:

inheritance, GCA, SCA, dominance, additive, genes, diallel and maize.

Received : 13 October 2024
Revised : 17 December 2024
Accepted : 30 December 2024
Published : 9 January 2025

Citation:

Maliha M. T., A. Hossain, M. Rahman, S. Islam, M. S. Alam, R. Khanam and M. S. Raihan. 2024. Genetic analysis of selected quantitative attributes in maize genotypes exploiting 6 × 6 diallel mapping population. *Ann. Bangladesh Agric.* 28(2): 137-153

ABSTRACT

Combining ability and heterosis for nine quantitative characters of six parental genotypes and 15 F_1s derived from a 6×6 diallel cross without reciprocal was assessed. Ranking of the parents for seventeen characters on general combining ability indicated that the parental genotype P3 was the best general combiner for plant height, number of kernels per cob, test weight and the genotype P6 for hundred kernel weight. The estimates of specific combining ability (SCA) effect revealed that in most of the cases, combinations of high × low or even low × low exhibited high SCA effect for many characters rather than high × high cross combinations indicating the importance of gene interaction. Based on SCA performances the hybrids H4 (P1×P5) and H13(P4×P5) were the best specific combiners for test weight. Test weight is the weight of a specific volume of grain. The hybrids H11, H5 and H15 were the best specific combiners for plant height, cob breath and number of kernels per row respectively. Heterosis was the highest in H4 (P1×P5) for mainly hundred kernel weight followed by H6 (P2×P3) over mid parent. The genetic analysis of maize genotypes using a 6 × 6 diallel cross revealed significant variation and combining abilities for key quantitative traits, offering a strong foundation for future hybrid breeding programs.

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https://doi.org/10.3329/aba.v28i2.77881

Introduction

Maize (*Zea mays* L.) is an incredibly adaptable crop, capable of thriving across a wide range of agro-climatic conditions. In eastern and southern Africa alone, it is cultivated on approximately 15 million hectares. However, the region commonly faces yield reductions due to diseases such as maize streak virus (MSV), grey leaf spot (GLS), and turcicum leaf blight (ET) (Vivek *et al*. 2010). Globally, maize is often referred to as the "Queen of Cereals" due to its exceptionally high yield potential among cereal crops. It serves multiple purposes providing food for humans, feed for poultry and fish, raw materials for various industries, and even biofuel (Britannica 2020).

In terms of global nutrition, maize alongside rice and wheat contributes significantly to the dietary calorie intake of nearly 4.5 billion people across 94 developing nations (CGIAR 2016). Virtually every part of the maize plant, from its grains to its leaves, stalks, tassels, and even pith, is utilized in producing both food and non-food products. In Bangladesh, maize became the most important cereal crop in 2016, overtaking rice and wheat. It is currently grown on 447,000 hectares with an average yield of 8 tons per hectare, and about 90% of its production is directed toward the growing poultry and aquaculture industries (The Daily Star 2019). Additive gene action was found to control traits like ear diameter, ear length, number of kernels per ear, and 100-grain weight, indicating that these traits can be improved through selection based on additive genetic variance (Aslam *et. al.* 2015). High genetic variability and heritability estimates were observed for traits like grain yield per plant, indicating a strong genetic control and potential for selection in breeding programs (Reddy *et. al.* 2023).

The diallel mating design is a valuable method in plant breeding, offering insight into the genetic mechanisms at work in early generations and assisting breeders in developing superior hybrids (Hayman 1954, Jinks 1954). Maize's prominence in global diets is partly due to its rich nutrient profile, which includes high carbohydrate levels along with essential proteins, oils, B vitamins, folic acid, vitamin C, provitamin A, and minerals such as phosphorus, magnesium, manganese, zinc, copper, and iron. It is also a good source of dietary fiber and protein while being low in fat and sodium. However, it lacks sufficient amounts of lysine and tryptophan two essential amino acids so it must be consumed as part of a balanced diet (Fulton *et al.* 2011).

Botanically, maize is a tall, annual grass with firm stems and long, narrow leaves that grow alternately on either side of the stem. The male flowers are borne on the terminal tassel, while the female inflorescences, which eventually develop into edible ears, are spike-like structures wrapped in protective husks (Britannica 2020). According to Vencovsky (1987), diallel crossing is particularly effective for estimating genetic parameters, offering breeders a sound basis for making selection decisions.

Understanding the genetic relationships among different crosses is crucial in breeding programs, as it helps identify the best combinations for achieving desired outcomes. Relying solely on physical appearance or phenotypic traits can be misleading. Combining ability analysis offers a powerful tool for assessing the genetic worth of parent lines and crosses, aiding in the identification of promising materials for further improvement (Singh *et al.* 2007). Several researchers have elaborated on these analytical techniques and provided illustrative examples in their publications (Mather and Jinks 1987, Singh and Chaudhary 1985, Dabholkar 1982, Narain 1993, Falconer and Mackay 1996). To harness the full potential of hybrid vigor, it is essential to identify parent genotypes with strong combining abilities. Diallel analysis is instrumental in this context, as it helps quantify both general combining ability (GCA), which reflects additive gene effects, and specific combining ability (SCA), which captures non-additive interactions such as dominance and epistasis (Cruz and Regazzi 1994). The objective of this study is to estimate the genetic variability, combining ability and heterosis among six selected maize genotypes for important quantitative traits.

Materials and Methods

Site selection for research materials

The experiment was carried out at the field laboratory of the Department of Genetics and Plant Breeding, Gazipur Agricultural University, Salna, Gazipur. The soil type of the experimental field belongs to the Shallow Red Brown Terrace type characterized by silty clay with pH value of 6.5 (Haider *et al.* 1991). The climate of the experimental site is subtropical in nature characterized by heavy rainfall during the months from June to September and scanty in winter with gradual fall of temperature from the month of September. Six genotypes of maize viz. 1,2,3,4,5 and 6 and their 15 F_1s derived from diallel cross (without reciprocal) were included in the experiment.

Selection of the genotypes

The materials used in the experiment were obtained through the germplasm pool of the Department of Genetics and Plant Breeding, GAU, Salna, Gazipur-1706. The parents were crossed in a half diallel, thus producing 15 F_1 progenies. All the mature F_1 seeds generated from crosses were harvested and dried up to 14% moisture content and stored for evaluating the generated progeny with their parents.

Experimental design and cultural practices for progeny evaluation

After raising seedlings in pots, single seedling per hill of all genotypes were transplanted to the experimental plot and five hills were assigned for one genotype P1 in a replication with an interspace of 20 cm. The genotypes were evaluated in a Randomized Complete Block Design (RCBD) with three replications having plant to plant and line to line distance of 20 cm and 20 cm, respectively. Standard intercultural practices were followed during cropping period for proper growth and

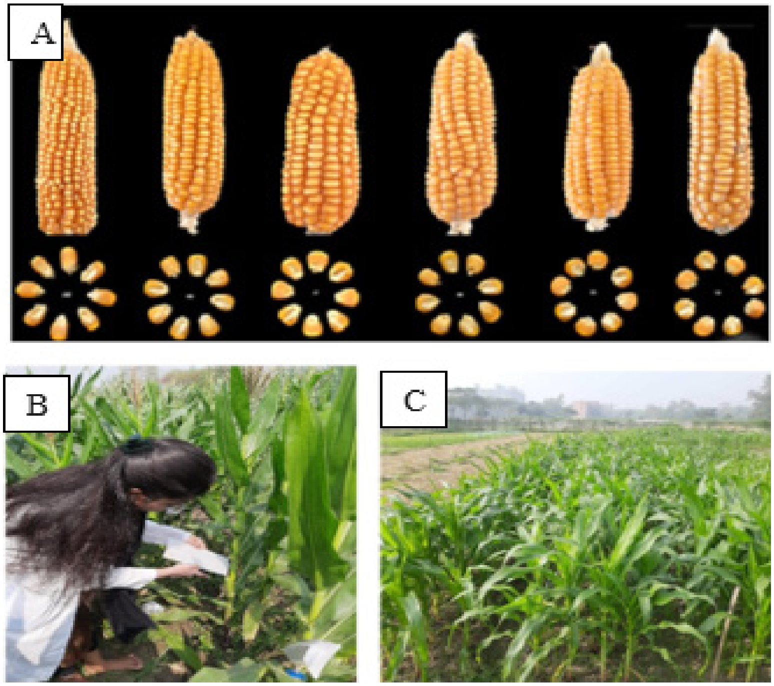

Fig. 1. Maize hybridization Program A)Selection of parents B) Development of experimental hybrids C) Evaluation of hybrids in the field.

development of the plants. Weeding, during first two top dressing of urea, was done to break the soil crust, to keep the plots free from weed and to incorporate the urea fertilizer into the soil for reducing the loss of urea through denitrification. Irrigation with regular interval was given to maintain 5-7 cm water up to hard dough stage of the maize. Proper control measures were taken against fall armyworm during vegetative stage of growth period of maize. Harvesting was done depending upon the maturity of different genotypes. Different genotypes attain their maturity at different times. The date of harvesting was confined when 90% of the grain attained golden yellow color.

Data collection and observations

Table 1 shows the traits and their measuring process. Data were recorded on individual plant basis from 10 randomly selected plants of each genotype. Among the studied characters plant height, stem diameter, no. of leaf at pollination were recorded in the field. The remaining characters were recorded in the field laboratory after harvesting. The data were collected on the traits as cob breadth (cm), cob weight (g), number of kernels per row, number of kernels per cob, husk weight (g), test weight and hundred kernel weight (g).

Table 1. Ten different traits with their measuring procedure

Trait	Measuring Procedure
Plant Height	Measure from soil surface to the top of the plant using a measuring tape.
Stem Diameter	Measure stem thickness at 5 cm above ground using a vernier caliper.
Number of Leaves at Pollination	Count the total number of fully expanded leaves manually.
Cob Breadth (cm)	Measure cob diameter at the middle using a vernier caliper after harvest.
Cob Weight (g)	Weigh each cob on a digital balance immediately after harvest.
Number of Kernels per Row	Count kernels in a single representative row on the cob.
Number of Kernels per Cob	Count total kernels on the entire cob manually or using a counting machine.
Husk Weight (g)	Weigh the husk removed from the cob on a digital balance.
Test Weight (g)	Weigh a standard quantity (e.g., 1000 kernels) and record the weight.
Hundred Kernel Weight (g)	Randomly pick and weigh 100 kernels using a digital balance.

Data observation and analysis

The preliminary statistical analysis of the data was done according to standard texts and the subjects (Snedecor and Cochran 1967, Clark 1973). For the genetic analysis of diallel population (F_1), data were subjected to Hayman's approach.

The analysis of variance for the complete diallel table was given by Hayman (1954a), developing in one direction that of Yates (1947). However, reciprocal differences are assumed absent, and only one of each pair of reciprocal crosses is raised. For such situation Morley Jones (1965) brought some modification of Hayman's approach (Table 1). In this modification using the same model as Hayman, the determination of the sum of squares corresponding to additive effects (a), and on the assumption of no epistasis to mean dominace (b_1), to additional dominance effects that can be accounted for by genes having one allele present in only one line (b_2) and to residual dominance effects (b_3), is in essence a straight forward application of fitting constants by least squares.

Results and Discussion

Mean Performance of the Parents and Hybrids

The mean values of various plant characters of parental genotypes and their hybrids (F_1s) are presented in Table-2 and the corresponding

The mean values of various plant characters of parental genotypes and their hybrids (F_1s) are presented in Table 2 and the corresponding analysis of variances (ANOVA) in table Table

4. Mean values of the parents and hybrid combinations (Table 3) revealed that the plant height ranges from 177.7cm in P4 to 232.4cm P1 and 190.5cm in H14 to 233.6cm in H6. The highest cob was observed in P6 (89.33cm) and the lowest in P2 (57.25cm) and most of the hybrids showed moderate cob height except H9. The highest kernel found in H5 (786). Considering kernel related traits, the longest kernel (12.62mm) was in H5 and the shortest kernel (10.62mm) in H2, the widest kernel 10.9mm in H12 and most limited 7.9mm in H5. The kernel with highest thickness was found in H5 (6.13mm) and lowest thickness (4.73mm) were found in H14.

Table 2. Mean values of different quantitative characters of the parents and hybrids of 6×6 diallel cross of Maize

				GCA Effects of Parents					
Genotype	PHT	SDR	NLP	CBT	NKR	NKC	HWT	KTW	HKW
P1	232.4	2.27	15	5.2	16	548	29.5	79.95	36.1
P2	221.3	2.17	13	5.49	18	486	33.63	78	38.33
P3	229.5	2	12	4.35	14	239	35.6	81.92	37.45
P4	177.7	1.33	14	4.31	11	233	22.82	79.2	36.8
P5	186	1.3	12	4.89	16	409	14.51	77.7	29.6
P6	215.2	1.5	13	4.73	11	322	30.88	73.48	43.04
				Hybrids					
H1(P1xP2)	218.5	2.1	12	5.17	16	503	30.2	76.34	35.52
H2(P1XP3)	231.8	2.33	15	4.58	16	398	30.7	82.47	21.95
H3(P1XP4)	199.6	2.4	16	4.7	14	434	25.72	85.42	37.15
H4(P1XP5)	208.8	2.6	14	4.65	14	448	23.2	86.52	46.2
H5(P1XP6)	203	2.3	14	5.57	18	786	40.05	78.3	34.8
H6(P2XP3)	233.6	2.36	13	5.21	16	446	42	79.4	43.3
H7(P2XP4)	228.6	2.4	15	5.02	14	493	41.6	77.8	40.16
H8(P2XP5)	204.2	2.42	13	5.1	17	552	35.9	77.45	36.72
H9(P2XP6)	204	1.47	13	4.98	14	436	24	81.2	43.45
H10(P3XP4)	208.2	2.1	13	4.8	15	387	39.08	83.43	38.31
H11(P3XP5)	198	2.4	13	5.3	18	521	25.44	69.45	34.68
H12(P3XP6)	206	1.93	14	4.88	12	377	28.64	78.44	47
H13(P4XP5)	227.2	2.42	14	4.82	18	456	37.1	87.34	33.8
H14(P4XP6)	190.5	2.47	12	4.55	12	342	26.92	80.1	40.2
H15(P5XP6)	201	2.72	12	5	14	523	44.36	76.22	39.66

Note: PHT=Plant Height (cm), SDR=Stem Diameter (cm), NLP= Number of Leaf at Pollination, CBT=Cob Breadth (cm), NKR= Number of Kernel per Row, NKC= Number of Kernel per Cob, HWT= Husk Weight (g), KTW= Kernel Test Weight (g), HKW= Hundred Kernel Weight (g).

Table 3. Analysis of variance (ANOVA) for different plant characters in a 6×6 diallel cross of Maize

Item	df	PHT	SDR	NLP	CBT	NKR	NKC	HWT	KTW	HKW
GCA	5	490.18**	0.07**	2.45**	0.22**	10.53**	24313.34**	38.10**	18.25**	26.11**
SCA	15	186.21**	0.20**	0.99**	0.08**	3.21**	10728.23**	65.65**	17.42**	18.09**
GCA:SCA		2.63:1	0.35:1	2.47:1	2.75:1	3.28:1	2.26:1	0.58:1	1.04:1	1.44:1

Note: PHT=Plant Height (cm), SDR=Stem Diameter (cm), NLP= Number of Leaf at Pollination, CBT=Cob Breadth (cm), NKR= Number of Kernel per Row, NKC= Number of Kernel per Cob, HWT= Husk Weight (g), KTW= Kernel Test Weight (g), HKW= Hundred Kernel Weight (g) **P<0.05, **P<0.01, ns= non-significant.

The analysis of variance (Table 3) showed that the mean squares for the genotypes of single cross hybrid parents were significant at P≤1 for all the characters studied.

The mean sum of squares of genotypes were highly significant for the characters such as plant height (cm), cob height, number of rows per cob, kernel per row, kernel per cob, hundred grains weight (g), test weight (g/50ml), kernel length (mm), kernel width (mm) and kernel thickness (mm). The significant variation among the values of the traits signified the existence of divergence and genetic variation among individuals (Chauhan *et al.,* 2019). Importantly, the highly significant mean sum of squares at 5 degrees of freedom (*df)* indicated the possibility of heterosis for the traits.

ANOVA for GCA and SCA Analysis

Table 4 presents the analysis of variance (ANOVA) results for the quantitative traits evaluated among the tested genotypes. All statistical analyses of several traits demonstrated considerable variance for all diallel cross features. Plant height (cm), number of kernels per row, number of kernels per cob, hundred kernel weight (g), test weight (g/100ml) were highly significant (**P<1). Ferdoush *et. al., (*2017) also found highly significant variation for plant height (cm), cob height (cm), cob length (cm), cob width (cm), number of kernels per cob and 1000-kernel weight (g). In another study Javid and Ahmed, (2014) claimed that number of rows per cob, number of kernels per row and 100 kernel weight also possess significant variation.

Combining Ability Analysis

The results of the analysis of combining ability variations for the six diallel hybrids of *Zea mays* are presented in Table 4. Tables 4 and 5 provide the estimates of general combining ability (GCA) and specific combining ability (SCA) effects of parents and their F_1s, respectively.

In combining ability analysis, parents were categorized into (i) good combiners for the highest GCA effects; (ii) poor combiners for the lowest value of GCA effects; (iii) average

Table 4. Analysis of variance (ANOVA) of combining ability for different plant characters in a 6×6 diallel cross of Maize

Source of variations	df	Mean Sum of Square								
		PHT	SDR	NLP	CBT	NKR	NKC	HWT	KTW	HKW
Replication	1	377.18**	10.50**	41.99**	10.49**	41.95**	4002.11**	41.99**	41.95**	41.96**
Genotype	20	524.37**	0.34**	2.71**	0.23**	10.09**	28249.02**	117.54*	35.25**	40.19**
Error	20	0.04	0	0	0	0	2.39	0.03	0.02	0.01

Note: PHT=Plant Height (cm), SDR=Stem Diameter (cm), NLP= Number of Leaf at Pollination, CBT=Cob Breadth (cm), NKR= Number of Kernel per Row, NKC= Number of Kernel per Cob, HWT= Husk Weight (g), KTW= Kernel Test Weight (g), HKW= Hundred Kernel Weight (g) $^{**}P<0.05$, $^{*}P<0.01$, ns= non-significant.

combiners for those having moderate GCA effects between the highest and the lowest values. The importance of additive gene activity was proven by the GCA:SCA ratio (Table 3). Because additive genetic variation predominates in this feature, the parent could be chosen based on GCA values. The predominance of traits for 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<1) 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. As a result, two factors are considered important for evaluating an inbred line in the production of hybrid maize.

General Combining Ability (GCA) Effects

The GCA effects of parental single cross hybrid lines for nine characters are shown in Table 5. A wide range of variability of GCA effects was observed among the parents. In the present study, plant height, cob height of the parental lines with significant and negative GCA effects were considered as good general combiners. Significant and negative GCA effects for plant height and cob height suggested that using these parents may be beneficial in developing early-maturing and short-statured hybrid varieties. On the other hand, for yield and other yield components those with significant and positive GCA effects were considered as good general combiners (Begum *et al.,* 2018). In this study, yield and yield contributing main traits were number of kernels per rows, kernel test weight, hundred kernel weight, etc.

P4 showed significant and negative GCA effect for the traits plant height (-8.19cm) indicating its potentiality for developing

Table 5. Estimates of general combining ability (GCA) effects for different plant characters in a 6×6 diallel cross of Maize

	GCA Effects of Parents								
Genotype	PHT	SDR	NLP	CBT	NKR	NKC	HWT	KTW	HKW
P1	6.43**	0.16**	0.88**	0.08**	0.67**	69.00**	-1.47**	1.53**	-1.28**
P2	7.06**	0.01**	-0.25**	0.25**	1.04**	36.13**	2.54**	-1.06**	0.97**
P3	7.70**	0.02**	-0.25**	-0.12**	0.04**	-63.25**	2.06**	0.04**	0.26**
P4	-8.19**	-0.07**	0.50**	-0.24**	-1.21**	-66.88**	-0.57**	1.97**	-0.61**
P5	-7.98**	0.02**	-0.50**	0.03**	1.04**	25.63**	-3.20**	-0.54**	-2.23**
P6	-5.02**	-0.14**	-0.38**	0ns	-1.58**	-0.63ns	0.64**	-1.94**	2.89**

Note: PHT=Plant Height (cm), SDR=Stem Diameter (cm), NLP= Number of Leaf at Pollination, CBT=Cob Breadth (cm), NKR= Number of Kernel per Row, NKC= Number of Kernel per Cob, HWT= Husk Weight (g), KTW= Kernel Test Weight (g), HKW= Hundred Kernel Weight (g) *P<0.05, **P<0.01, ns= non-significant.

early and short stature hybrid variety(s). For most of the yield and yield contributing traits of parental line P1 showed significant and the highest positive effects of GCA. P1 was identified as a good combiner for exhibiting significant and highest GCA effects for number of kernels per cob (69), number of kernels per row (0.67). For number of kernels per cob P1 exhibited the highest positive and significant GCA effects (69) followed by P2 (36.13). In case of test weight/100 ml P4 (1.97) and P1 (1.53) exhibited the highest GCA effect which is considered as one of the most important criterions for hybrid development. P2 and P6 were good combiners for 100 kernel weight with GCA effect 0.97 and 2.89 respectively. So, considering all yield contributing traits P1 parental line showed better result than any other parental line.

Specific Combining Ability (SCA) Effects

The estimates of specific combining ability (SCA) effects in the 15 F_1 crosses for the studied traits are given in Table 6. For cob breath H5 (0.57) showed the highest and positive SCA effects followed by H11 (0.47). For stem diameter the highest SCA value was observed in H15 (P5×P6) which is 0.70 and statistically significant. Therefore, those hybrids seem to be suitable for plant height improvement. Similar results were obtained by (Muraya *et al.,* 2006; Alam *et al.,* 2008). Number of kernels per cob H5 (272.91) showed positive SCA effect than other hybrids. Hundred kernel weight H4 (11.41) showed the highest positive and significant value than other hybrids. Positive SCA is indicative of an increase in a given trait compared to the parents (Jatasra *et al.,* 1980; Kang *et al.*, 1995). For kernel yield, the

Table 6. Estimates of specific combining ability (SCA) effects for different plant characters in a 6×6 diallel cross of maize

	SCA Effects of Hybrids								
Genotype	PHT	SDR	NLP	CBT	NKR	NKC	HWT	KTW	HKW
H1(P1xP2)	-5.71**	-0.21**	-2.05**	-0.08**	-0.66**	-46.84**	-2.39**	-3.66**	-2.46**
H2(P1XP3)	6.95**	0.01**	0.95**	-0.30**	0.34**	-52.46**	-1.40**	1.37**	-5.32**
H3(P1XP4)	-9.36**	0.17**	1.20**	-0.06**	-0.41**	-12.84**	-3.76**	2.39**	0.74**
H4(P1XP5)	-0.37**	0.28**	0.20**	-0.38**	-2.66**	-91.34**	-3.65**	6.00**	11.41**
H5(P1XP6)	-9.14**	0.14**	0.07**	0.57**	3.96**	272.91**	9.36**	-0.82**	-5.10**
H6(P2XP3)	8.13**	0.19**	0.07**	0.16**	-0.04**	28.41**	5.89**	0.90**	3.78**
H7(P2XP4)	19.01**	0.31**	1.32**	0.09**	-0.79**	79.04**	8.11**	-2.64**	1.50**
H8(P2XP5)	-5.60**	0.25**	0.32**	-0.10**	-0.04**	45.54**	5.04**	-0.47**	-0.32**
H9(P2XP6)	-8.76**	-0.55**	0.20**	-0.19**	-0.41**	-44.21**	-10.7**	4.67**	1.30**
H10(P3XP4)	-2.02**	0.01**	-0.68**	0.24**	1.21**	72.41**	6.08**	1.89**	0.36**
H11(P3XP5)	-12.44*	0.22**	0.32**	0.47**	1.96**	113.91**	-4.93**	-9.58**	-1.65**
H12(P3XP6)	-7.40**	-0.09**	1.20**	0.08**	-1.41**	-3.84**	-5.57**	0.81**	5.56**
H13(P4XP5)	32.65**	0.33**	0.57**	0.11**	3.21**	52.54**	9.35**	6.38**	-1.66**
H14(P4XP6)	-7.01**	0.53**	-1.55**	-0.13**	-0.16**	-35.21**	-4.67**	0.53**	-0.38**
H15(P5XP6)	3.28**	0.70**	-0.55**	0.05**	-0.41**	53.29**	15.40**	-0.83**	0.70**

Note: PHT=Plant Height (cm), SDR=Stem Diameter (cm), NLP= Number of Leaf at Pollination, CBT=Cob Breadth (cm), NKR= Number of Kernel per Row, NKC= Number of Kernel per Cob, HWT= Husk Weight (g), KTW= Kernel Test Weight (g), HKW= Hundred Kernel Weight (g) $*P<0.05$, $**P<0.01$, ns= non-significant.

best SCA effects were significantly positive. These hybrids also had the highest combined analysis values. It could be concluded that the parental inbred line for those crosses could make themselves recombined. Similar results were obtained by (Muraya *et al.,* 2006).

Heterosis studies

Heterosis was estimated for individual crosses i.e. 15 single cross hybrid maize for nine characters over mid-parent (MP) and better parent (BP) and standard parent (SP) presented in Table 7.

Positive values ratio denoted degrees of dominance, ranging from partial to over-dominance, whereas negative values ratio denoted degrees of recessiveness, ranging from partial to under-recessiveness (Solieman *et al.,* 2013; Begum *et al.,* 2017).

Table 7. Heterosis over mid parent (MP), better parent (BP) and standard parent (SP) for different plant characters in a 6×6 diallel cross of Maize

	PHT			SDR		
Genotype	MP	BP	SP	MP	BP	SP
H1(P1xP2)	-3.68**	-5.98**	-5.98**	-5.41**	-7.49**	-7.49**
H2(P1xP3)	0.37**	-0.26**	-0.26**	9.13**	2.64**	2.64**
H3(P1xP4)	-2.66**	-14.11**	-14.11**	33.33**	5.73**	5.73**
H4(P1xP5)	-0.19*	-10.15**	-10.15**	45.66**	14.54**	14.54**
H5(P1xP6)	-9.29**	-12.65**	-12.65**	22.02**	1.32**	1.32**
H6(P2xP3)	3.64**	1.79**	0.52**	13.19**	8.76**	3.96**
H7(P2xP4)	14.59**	3.30**	-1.64**	37.14**	10.60**	5.73**
H8(P2xP5)	0.27**	-7.73**	-12.13**	39.48**	11.52**	6.61**
H9(P2xP6)	-6.53**	-7.82**	-12.22**	-19.89**	-32.26**	-35.24**
H10(P3xP4)	2.26**	-9.28**	-10.41**	26.13**	5.00**	-7.49**
H11(P3xP5)	-4.69**	-13.73**	-14.80**	45.45**	20.00**	5.73**
H12(P3xP6)	-7.35**	-10.24**	-11.36**	10.29**	-3.50**	-14.98**
H13(P4xP5)	24.94**	22.15**	-2.24**	84.03**	81.95**	6.61**
H14(P4xP6)	-3.03**	-11.48**	-18.03**	74.56**	64.67**	8.81**
H15(P5xP6)	0.20*	-6.60**	-13.51**	94.29**	81.33**	19.82**
H1(P1xP2)	-14.29**	-20.00**	-20.00**	-3.27 **	-5.83 **	-0.58 **
H2(P1xP3)	11.11 **	0 ns	0 ns	-4.08 **	-11.92 **	-11.92 **
H3(P1xP4)	10.34**	6.67**	6.67**	-1.16 **	-9.62 **	-9.62 **
H4(P1xP5)	3.7**	-6.67**	-6.67**	-7.83 **	-10.58 **	-10.58 **
H5(P1xP6)	0 ns	-6.67**	-6.67**	12.19 **	7.12 **	7.12 **
H6(P2xP3)	4**	0 ns	-13.33**	5.89 **	-5.10 **	0.19 *
H7(P2xP4)	11.11**	7.14**	0 ns	2.45 **	-8.56 **	-3.46 **
H8(P2xP5)	4.00**	0 ns	-13.33**	-1.73 **	-7.1 **	-1.92 **
H9(P2xP6)	0 ns	0 ns	-13.33**	-2.54 **	-9.29 **	-4.23 **
H10(P3xP4)	0 ns	-7.14**	-13.33**	10.85 **	10.34 **	-7.69 **
H11(P3xP5)	8.33**	8.33**	-13.33**	14.72 **	8.38 **	1.92 **
H12(P3xP6)	12.00**	7.69**	-6.67**	7.49 **	3.17 **	-6.15 **
H13(P4xP5)	7.69**	0 ns	-6.67**	4.78 **	-1.43 **	-7.31 **
H14(P4xP6)	-11.11**	-14.29**	-20.00**	0.66 **	-3.81 **	-12.50 **
H15(P5xP6)	-4.00**	-7.69**	-20.00**	3.95 **	2.25 **	-3.85 **
H1(P1xP2)	-5.88 **	-11.11 **	0 ns	-2.71 **	-8.21 **	-8.21 **
H2(P1xP3)	6.67 **	0 ns	0 ns	1.14 **	-27.37 **	-27.37 **
H3(P1xP4)	3.70 **	-12.50 **	-12.50 **	11.14 **	-20.80 **	-20.8 **

Table 7. (Contd.)

		PHT			SDR	
Genotype	MP	BP	SP	MP	BP	SP
H4(P1xP5)	-12.50**	-12.50 **	-12.50 **	-6.37 **	-18.25 **	-18.25 **
H5(P1xP6)	33.33 **	12.50 **	12.50 **	80.69 **	43.43 **	43.43 **
H6(P2xP3)	0 ns	-11.11 **	0 ns	23.03 **	-8.23 **	-18.61 **
H7(P2xP4)	-3.45 **	-22.22 **	-12.50 **	37.13 **	1.44 **	-10.04 **
H8(P2xP5)	0 ns	-5.56 **	6.25 **	23.35 **	13.58 **	0.73 *
H9(P2xP6)	-3.45 **	-22.22 **	-12.50 **	7.92**	-10.29 **	-20.44 **
H10(P3xP4)	20.00 **	7.14 **	-6.25 **	63.98 **	61.92 **	-29.38 **
H11(P3xP5)	20.00 **	12.50 **	12.50 **	60.80 **	27.38 **	-4.93 **
H12(P3xP6)	-4.00 **	-14.29 **	-25.00 **	34.40 **	17.08**	-31.20 **
H13(P4xP5)	33.33 **	12.50 **	12.50 **	42.06 **	11.49 **	-16.79 **
H14(P4xP6)	9.09 **	9.09 **	-25.00 **	23.24 **	6.21 **	-37.59 **
H15(P5xP6)	3.70 **	-12.50 **	-12.5 **	43.09 **	27.87 **	-4.56 **
H1(P1xP2)	-4.32 **	-10.2 **	2.37 **	-3.34 **	-4.52 **	-4.52 **
H2(P1xP3)	-5.68 **	-13.76 **	4.07 **	1.90 **	0.67 **	3.15 **
H3(P1xP4)	-1.68 **	-12.81 **	-12.81 **	7.35 **	6.84 **	6.84 **
H4(P1xP5)	5.43 **	-21.36 **	-21.36 **	9.76 **	8.22 **	8.22 **
H5(P1xP6)	32.66 **	29.7 **	35.76 **	2.07 **	-2.06 **	-2.06 **
H6(P2xP3)	21.33 **	17.98 **	42.37 **	-0.70 **	-3.08 **	-0.69 **
H7(P2xP4)	47.39 **	23.70 **	41.02 **	-1.02 **	-1.77 **	-2.69 **
H8(P2xP5)	49.15 **	6.75 **	21.69 **	-0.51 **	-0.71 **	-3.13 **
H9(P2xP6)	-25.59 **	-28.64 **	-18.64 **	7.21 *	4.10 **	1.56 **
H10(P3xP4)	33.79 **	9.78 **	32.47 **	3.56 **	1.84 **	4.35 **
H11(P3xP5)	1.54 **	-28.54 **	-13.76 **	-12.98 **	-15.22 **	-13.13 **
H12(P3xP6)	-13.84 **	-19.55 **	-2.92 **	0.95 **	-4.25 **	-1.89 **
H13(P4xP5)	98.77 **	62.58 **	25.76 **	11.33 **	10.28 **	9.24 **
H14(P4xP6)	0.26 **	-12.82 **	-8.75 **	4.93 **	1.14 **	0.19 **
H15(P5xP6)	95.46 **	43.65 **	50.37 **	0.83 **	-1.9 **	-4.67 **

Table 7. (Contd.)

	HKW		
Genotype	**MP**	**BP**	**SP**
H1(P1xP2)	-4.55 **	-7.33 **	-1.61 **
H2(P1xP3)	-13.12 **	-14.69 **	-11.50 **
H3(P1xP4)	1.92 **	0.95 **	2.91 **
H4(P1xP5)	40.64 **	27.98 **	27.98 **
H5(P1xP6)	-12.05 **	-19.14 **	-3.60 **
H6(P2xP3)	14.28 **	12.97 **	19.94 **
H7(P2xP4)	6.91 **	4.77 **	11.25 **
H8(P2xP5)	8.11 **	-4.20 **	1.72 **
H9(P2xP6)	6.80 **	0.95 **	20.36 **
H10(P3xP4)	3.19 **	2.30 **	6.12 **
H11(P3xP5)	3.45 **	-7.40 **	-3.93 **
H12(P3xP6)	16.78 **	9.20**	30.19 **
H13(P4xP5)	1.81 **	-8.15 **	-6.37 **
H14(P4xP6)	0.70 **	-6.60 **	11.36 **
H15(P5xP6)	9.20 **	-7.85 **	9.86 **

Note: PHT=Plant Height (cm), SDR=Stem Diameter (cm), NLP= Number of Leaf at Pollination, CBT=Cob Breadth (cm), NKR= Number of Kernel per Row, NKC= Number of Kernel per Cob, HWT= Husk Weight (g), KTW= Kernel Test Weight (g), HKW= Hundred Kernel Weight (g), MP= Mid Parent, BP=Better Parent, SP= Standard Parent *P<0.05, **P<0.01, ns= Non-significant.

Plant Height (cm)

Highly significant (**P<0.01) heterosis based on average of all parents and all hybrids was observed for this trait. The extent of significantly heterosis over mid-parent (MP) ranged from -9.29% to 24.94% while no cross was found non-significant for mid parents heterosis in Table 7. Significant heterosis in negative direction over MP was found in this trait. Heterosis over better parent (BP) ranged from -14.11% to 22.15% depending on the crosses. The highest negative heterosis for plant height was recorded in the H3 (-14.11cm) followed by H11 (-13.73%). Therefore, H3 could be considered as the most promising for this trait.

Stem Diameter

Positive heterosis is desirable for diameter related traits. The lowest and highest heterosis over MP was reported for H9 (P2×P6) and H15 (P5×P6) which were -19.89% and 94.29%, respectively. The heterosis over BP ranged from -32.26% for H9 (P2×P6) to 81.95% for H13 (P4×P5). Two crosses viz. P1×P2 and P2×P6 out of 15 crosses exhibited negative heterosis over MP both of which are significant.

Number of Leaves at Pollination

Positive heterosis is desirable for this trait. The lowest and highest significant heterosis over MP was reported for H1 (P1×P2) and H12 (P3×P6) which were -14.29% and 12.00%, respectively. The heterosis over BP ranged from -20.00% for H1 (P1×P2) to 8.33% for H11 (P3×P5). Three crosses viz. P1×P2, P4×P6 and P5×P6 out of 15 crosses exhibited negative heterosis where all of them are significant. On the contrary, six crosses out of fifteen crosses exhibited negative heterosis over BP and all of them are significant.

Cob Breadth

Positive heterosis is desirable for breadth related traits. The lowest and highest heterosis over MP were reported for H4 (P1×P5) and H11 (P3×P5) which were -7.83% and 14.72%, respectively. The heterosis over BP ranged from -11.92% for H2 (P1×P3) to 10.34% for H10 (P4×P5). Six crosses out of 15 crosses exhibited negative heterosis over MP which all are significant.

Number of Kernels per Row

Positive heterosis is desirable for kernel related traits. Positive heterosis over mid-parent was observed for 11 hybrids out of 15 and among them H5 (33.33%), H13 (33.33%) and H10 (20%) were appeared to be the most desirable due to their highest positive heterotic effect. Heterosis over better parent (BP) ranged from -22.22% to 12.5% and almost crosses (9 out of 15 crosses) exhibited positive heterosis over BP. Thus, the expression of heterosis for kernel per row was far wide. The highest positive heterosis (12.5%) over BP was recorded in the H13, whereas the hybrid H11 (12.5%) and H5 (12.5%) also exhibited good results.

Number of Kernels per Cob

The lowest and highest heterosis over mid-parental value for individual crosses were -6.37% for H4 and 80.69% for H5. No negative heterosis was observed for heterosis over mid parents (MP). The range of heterosis over BP were 27.87% to -27.37%, the lowest and highest estimates were H1 and H15, respectively. Frascaroli *et. al.,* (2007) also observed varying levels of heterosis for total kernels per cob in F_1 studies.

Husk Weight

Negative heterosis is desirable for this trait. The lowest and highest significant heterosis over MP was reported for H9 (P2×P6) and H13 (P4×P5) which were -25.59% and 98.77%, respectively. The heterosis over BP ranged from -28.64% for H9 (P2×P6) to 62.58% for H13 (P4×P5). On the contrary, eight crosses out of fifteen crosses exhibited negative heterosis over BP and all of them are significant.

Hundred Kernel 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 exception of three hybrids (H1, H2 and H5) that were negatively significant. The lowest and highest heterosis over mid parent (MP) was recorded H2 (-13.12%) and H4 (40.64%), respectively. The extent of heterosis over better parent (BP) ranged from -19.145 to 27.98% Significant positive heterosis was showed by 7 crosses out of 15 crosses. Myraya *et. al.* (2006) and Devi *et. al.* (2007) who observed varying degree of heterosis for 100 grain weight in F1 studies.

Kernel Test Weight (g/100ml)

A cross will be preferable alternative for hybrid maize production in the future due to its high significant test weight. Heterosis over mid parent ranged from H11 (-12.98%) to H13 (11.33%). Negative heterosis was found in five crosses out of 15 crosses over mid parent. Over better parent heterosis ranged from -15.22% to 10.28%. The highest positive heterosis was recorded for the hybrid H13 (10.28%) followed by hybrid H3 (6.84%). Therefore, hybrid H13 (10.28%) as well as H3 (6.84%) could be considered as the most promising for this trait.

Conclusion

The GCA and SCA variance were found highly significant for all the characters except for number of kernels per row, test weight and hundred kernel weight which revealed the importance of both additive and non-additive gene action. The parent P3 was found to be the best desirable general combiner considering kernel related traits and it was also desirable for plant height and cob breadth. The hybrids namely H3, H5 and H11 were the best specific combiners for plant height, cob breadth and number of kernels per row respectively. For hundred kernel weight, the hybrid H4 demonstrated significant heterosis over the better parent.

Acknowledgement

The project was partially supported by the Research Management Committee (RMC) grant of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Bangladesh (2021-2024: Project No.: 09)

Author’s Contribution: All authors contributed significantly to the research and preparation of the manuscript. The first author led the experimental design, data collection, statistical analysis, field management, data interpretation, and literature review. The corresponding author supervised the entire research process and contributed to manuscript editing and final approval. All authors reviewed and approved the final version for submission.

Conflict of Interest: The authors declare that there is no conflict of interest regarding the publication of the research paper. All research activities were conducted independently, without any commercial or financial relationships that could be construed as a potential conflict.

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